

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model
Run on: June 15, 2003, 21:11:36 ; Search time 2164.55 seconds
(without alignments)
3925.989 Million cell updates/sec

US-09-624-670-63
Title: 1567
Sequence: 1 MEOLKAFDNEVNAFLDNNMFG.....NGPKNAHLIVANGMTDKKAAQ 292

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
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Searched: 2054640 seqs, 14551402878 residues
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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39: em_htgo_hum.*
40: em_htgo_mus.*
41: em_htgo_other.*

pred No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1567	100.0	3708	10	AF170908	AF170908 Mus muscu
3	1567	100.0	3795	6	AX052773	AX052773 Sequence
4	1430	91.3	2340	9	AK000341	AK000341 Homo sapi
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6	958.5	61.2	900	10	AB071985	AB071985 Rattus no
7	956.5	61.0	900	6	AX464735	AX464735 Sequence
8	951.5	60.7	2757	9	HS0801903	HS0801903 Homo sapi
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14	910	58.1	1397	5	AF455250	AF455250 Scophthal
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21	679	43.3	383	6	AX402493	AX402493 Sequence
22	679	43.3	3415	6	AF277093	AF277093 Mus muscu
23	663.5	42.6	28539	14	AF198100	AF198100 Fowlpox v
24	621	33.9	846	6	AX467489	AX467489 Sequence
25	531.5	33.5	1986	3	AY119173	AY119173 Drosophila
26	525.5	33.1	2580	3	AY060267	AY060267 Drosophila
27	495	31.8	86294	5	AC095019	AC095019 Rattus no
28	495	31.6	2508	9	AK027216	AK027216 Homo sapi
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37	457.5	29.2	1471	9	AF336793	AF336793 Homo sapi
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40	453	28.9	1471	9	AF151846	AF151846 Homo sapi
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42	419.5	26.8	173781	3	AC096692	AC096692 Drosophila
43	419.5	26.8	173781	3	AC096692	AC096692 Drosophila
44	419.5	26.8	281602	3	AF003546	AF003546 Drosophila
45	407.5	26.0	50374	2	AC015170	AC015170 Drosophila

ALIGNMENTS

us-09-624-670-63.1rg

Mon Jun 16 09:01:11 2003

DEFINITION

Sequence 5 from Patent WO0070945.

AX052773

AX052773.1 G1:12226935

KEYWORDS

Mus sp.

ORGANISM

Mus sp.

REFERENCE

1 (bases 1 to 3795)

AUTHORS

Jacobsson, A.T., Asadi, A.T., Westerberg, R.T., Nedergaard, J.T. and

Tvardik, P.M.

TITLE

Fatty acid elongation genes and uses thereof

JOURNAL

Patent: WO 0070945-A 5 30 NOV 2000,

Karolinska Innovations AB (SE)

FEATURES

Location/Qualifiers

1..3795

/organism="Mus sp."

/db_xref="taxon:10095"

BASE COUNT 1071 a 867 c 779 g 1078 t

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Best local similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 6 Gaps: 0

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Score: 1567.00 Matches: 292

Percent Similarity: 100.00% Conservativity: 0

Best local similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

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37 ATGAGCAGCTGAAGGCTTTGATATGAATGAATGCTTCTTGACACATGTTTGA 96

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97 CCAGCAGATTCTCGAGTTCGGGGTGGTTCCTGGAGCTCTTACCTTCCACCTTCATC 156

Db |||||||

41 LeuThrIleThrTyrLeuLeuSerIleTrpLeuGlyAsnLysTyrMetLysAsnArgPro 60

QY |||||||

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Db |||||||

61 AlaLeuSerLeuArgGlyIleLeuThrLeuTyrAsnLeuAlaIleThrLeuLeuSerAla 80

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217 GCT 276

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457 CAGATCAGCTTCT 516

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QY |||||||

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221 LeuSerAlaValValLysProCysGlyPheProPheGlyCysLeuIlePheGlnSerSer 240

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RESULT 3

AX052773

LOCUS

3795 bp DNA linear FAT 12 JAN 2001

[illegible]

Mammalia: Eutheria: Primates: Catarrhini: Hominoidea: Homo.

REFERENCE
AUTHORS Mukerji, P., Das T., Huang, Y.S., Parker-Barnes, J.M., Leonard, A.E.,
Thurmond, J., and Pereira, S.L.
TITLE Elouage genes and uses thereof
JOURNAL Patent: WO 02/04601 A3 31-JAN-2002
ABBOTT LABORATORIES (US)
FEATURES
location/qualifiers
L: 914
/organism="Homo sapiens"
/db xref="taxon:9606"
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US 09-624 670-63 (1-292) x AX464732 (1-914)

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QY 24 SerArgValArgGlyTyrPheLeuLeuAspSerTyrLeuProThrPheLeuThrLeu 43
DB 61 ACTAGAGTAAAGATGATGTTCTTCGCAATATATACCCACATTTATCTGCTCTGTC 120

QY 44 ThrTyrLeuLeuSerIleTyrPheLeuGlyAsnLysTyrMetLysAsnArgProAlaLeuSer 63
DB 121 ATATATTACTAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 190

QY 64 LeuArgGlyTyrLeuThrLeuTyrAsnLeuAlaIleThrLeuLeuSerAlaLysMetLeu 83
DB 181 TGGCGAGGATTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240

QY 84 ValGluLeuLeuLeuSerSerTyrPheGlyGlyTyrAsnLeuGlyGlyGlyGlyGlyGly 103
DB 241 TGTGAGTTAGTAAAGAGTAAAGAGTAAAGAGTAAAGAGTAAAGAGTAAAGAGTAAAG 300

QY 104 SerAlaGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 123
DB 401 AGCGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 360

QY 124 LeuValGluPheLeuAspThrIlePhePheValLeuArgLysLysLysLysLysLysLys 143
DB 361 CTCATAGAAATTTATGAGTAACTTCTCTCATCTGCGAGAGAGAGAGAGAGAGAGAGAG 420

QY 144 PheLeuHisValTyrHisHisAlaSerMetPheAsnIleTyrPheCysValLeuAsnTrp 163
DB 421 GTCTGCGAGTCACTATCACTATCACTATCACTATCACTATCACTATCACTATCACTAT 480

QY 164 IleProCysGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 183
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QY 224 ValValLysProGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 243
DB 661 GTCATCTGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 720

QY 244 ThrLeuValIleLeuPheLeuAsnPheTyrIleClnThrTyrArgLysLysProValLys 263

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QY 264 TysGlyLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 282
Db 741 GGAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 828

QY 283 AlaAsnGlyMetThrThrThrThrThrThrThrThrThrThrThrThrThrThrThr 288
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RESULT 12
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LOCUS 105465 Sequence 1 from Patent EP 028405.
ACCESSION 105465
VERSION 105465.1 GI:590717
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified
REFERENCE 1 (bases 1 to 2592)
AUTHORS Ishizaka, K., Martens, C.L., and Moore, K.W.
TITLE Glycosylation inhibition factors
JOURNAL Patent: EP 028405: A1 1 05 OCT 1988.
FEATURES
location/qualifiers
L: 2592
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BASE COUNT 684 a 575 c 548 g 785 t
ORIGIN

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US 09-624-670-63 (1-2592) x 105465 (1-2592)

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QY 153 MetPheAsnIleTyrTrpCysValLeuAsnTrpIlePheCysGlyGlySerPhePheGly 172
Db 430 ATCTCAACATCT 489



GenCore version 5.1.6
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QM protein - nucleic search, using frame_plus_p2n model

Run on: June 15, 2003, 20:25:36 ; Search time 201.384 seconds
(without alignments)
3262.066 Million cell updates/sec

Title: US-09-624-670-63

Perfect score: 1567
Sequence: 1 MEGLKAFUNEVNAFLDNMFG. NGFFKAHLIVANGMTDKKAO 292

Scoring table:
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Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
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Searched: 2185239 seqs, 112599459 residues

Total number of hits satisfying chosen parameters: 4370478

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Length	DB	ID	Description
1	1567	100.0	879	24	ABK46369	Mouse elongase MEL
2	1567	100.0	879	22	AAK91702	Mouse fatty acid e
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4	1431	91.3	3645	23	ABV24286	Human prostate exp
5	1431	91.3	3645	23	ABV28431	Human prostate exp
6	956.5	61.0	900	24	ABK46370	Mouse elongase MEL
7	951.5	60.7	2001	23	ABV23421	Human prostate exp
8	951.5	60.7	2001	23	ABV24778	Human prostate exp
9	951.5	60.7	2001	23	ABV25364	Human prostate exp
10	951.5	60.7	2001	23	ABV29278	Human prostate exp
11	951.5	60.7	2313	21	AAK94320	Human vesicle asso
12	951.5	60.7	2627	22	AAK94320	Human full-length
13	951.5	60.7	2769	22	AAK94320	Human full-length
14	951.5	60.7	3083	22	AAK94320	Human full-length
15	947.5	60.5	2710	21	AAK54132	Breast cancer prot
16	946.5	60.4	914	21	AAK54132	Human elongase HSE
17	941.5	60.1	914	24	ABK46367	Human elongase HSE
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20	749	47.8	748	22	AAK91702	cDNA encoding nove
21	741	47.3	680	22	AAK91702	Human cDNA 5'-end
22	741	47.3	680	22	AAK91702	Human cDNA clone r
23	691.5	44.1	975	22	AAK91702	Human cold-induced
24	679	43.3	972	24	AAK91702	Human elongation o
25	679	43.3	1203	23	AAK91702	DNA encoding novel
26	679	43.3	3383	24	ABK28654	Human MDR1 encodin
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33	506.5	32.3	1914	23	ABK91702	Drosophila melanog
34	476.5	30.4	881	23	ABK91702	Drosophila melanog
35	465	29.7	888	23	ABK91702	Drosophila melanog
36	464.5	29.6	1329	23	ABK91702	Human NF-KB activa
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38	462.5	29.5	1482	19	AAV59752	Human secreted pro
39	462.5	29.5	1514	24	AAV59752	Human secreted pro
40	462.5	29.5	1542	19	AAV59752	Human secreted pro
41	462.5	29.5	1566	21	AAV59752	Human transmembran
42	460.5	29.4	1457	22	AAH14551	Human cDNA sequenc
43	457.5	29.2	969	22	AAK91702	Human fatty acid e
44	457.5	29.2	1468	22	AAK91702	Mouse fatty acid e
45	455.5	29.1	1083	23	ABK91702	Drosophila melanog

ALIGNMENTS

RESULT 1
ID ABK46369 standard; cDNA, 879 BP.
XX
AC ABK46369;
XX
DT 05-JUN-2002 (first entry)
XX
DE Mouse elongase MEL04 cDNA.

ss: gene; elongase; polyunsaturated fatty acid; pufa; transgenic plant;
transgenic non-human animal; plant oil; arachidonic acid; nutritional;
pharmacut-cal; cosmetic; animal feed; testonosis; angioplasty; AIDS;
acquired immunodeficiency syndrome; multiple sclerosis; cachexia; asthma;
inflammatory skin disease; osteoporosis; kidney stone; cancer; eczema;
inflammation; rheumatoid arthritis; psoriasis; platelet aggregation;
vasodilation; cholesterol reduction; gastrointestinal bleeding.

CC (1) assessing the prostate cell carcinogenic potential of a compound;
 CC (4) determining whether prostate cancer has metastasized in a patient;
 CC (h) assessing the aggressiveness or indolence of prostate cancer in a patient;
 CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker.

XX Sequence 3645 BP: 1041 A: 793 C: 684 G: 1119 T: 8 other:

Alignment Scores:

Prod. No.: 5,360-139 Length: 3645
 Score: 1431.00 Matches: 262
 Percent Similarity: 93.92% Conservative: 16
 Best Local Similarity: 88.51% Mismatches: 14
 Query Match: 91.32% Indels: 4
 DB: 23 Gaps: 1

US-09-624-670-63 (1-292) x ABV28431 (1-3645)

QY 1 MetGluGlnLeuValAlaPheAspAsnGlyValAsnAlaPheLeuAspAsnMetPheGly 20
 DB ATGGAACATCTAAAGGCGCTTCATCATCAATCAAGCTTTTGGACAAATGCTTTGGA 144
 QY 21 PheArgAspSerArgValArgGlyTyrPheLeuLeuAspSerTyrLeuProThrPheLe 40
 DB CCGTGGAGATCTGATGATGAGAGATGTTTCAATTTGGAATTTTATTTTCTTCTTTT 284
 QY 41 LeuThrLeuThrTyrLeuLeuSerLeuThrPheGlyAsnGlyTyrMetLysAsnArgGlu 60
 DB CTATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 204
 QY 61 AlaLeuSerLeuArgGlyTyrLeuThrLeuTyrAsnLeuAlaLeuThrLeuLeuSerAla 80
 DB GCCTTTCTCTCAGGGGATGCTCAGCTTTGATTAATCTTGGAAATCAGACTTCTCTGGCG 324
 QY 81 TyrMetLeuValGlnLeuLeuSerSerTrpGluGlyTyrAsnLeuGlnGlyGln 100
 DB TACATGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 384
 QY 101 AsnLeuAspSerAlaGlyGluGlyAspValArgValAlaLysValLeuTrpTyrTyr 120
 DB GATCTTACCAGCGCAGCGCAGCGCAGCGCAGCGCAGCGCAGCGCAGCGCAGCGCAGCGC 444
 QY 121 PheSerLysLeuValGluPheLeuAspThrLeuPheValLeuArgLysLysThrAsp 140
 DB TCTCCAAATCAGTACAGTACAGTACAGTACAGTACAGTACAGTACAGTACAGTACAGTAC 504
 QY 141 GluLeuThrPheLeuHisValTyrHisHisAlaSerMetPheAsnLeuTrpTyrCysVal 160
 DB CAGATTACTTTCT 584
 QY 161 LeuAsnThrPheProCysGlyCysSerPheGlyProThrLeuAsnSerPheLeuHis 180
 DB TGAACATGATACCTTCT 624
 QY 181 ThrLeuMetTyrSerTyrTyrGlyGlySerValPheProSerMetLysLysTyrLeuTrp 200
 DB ATTCTTATCTACT 684
 QY 201 TrpLysLysTyrLeuThrGlnAlaLeuValGlnLeuValLeuThrThrHisThr 220
 DB TGAACATGATACCTTCT 744
 QY 221 LeuSerAlaValAlaLysProCysGlyPheProPheGlyCysLeuLeuPheGlnSerSer 240
 DB ATGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 804
 QY 241 TyrMetLeuThrLeuValLeuLeuPheLeuAsnPheTyrLeuGlnThrTyrArgLysLys 260
 DB TATATGCTAACCTTACTATCT 864
 QY 261 ProValLysLysLeuLeuGlnGlu-----LysGluValLysAsnGlyPhePro 276
 DB CCAATGAGAAAT 924

QY 277 LysAlaHisLeuValAlaAsnGlyMetThrAspLysLysAlaGln 292
 DB TTTTCT 972

RESULT 5

ABV28431
 ID ABV28431 standard: cDNA: 3645 BP.

XX AC ABV28431;
 XX CT 16-SEP-2002 (first entry)
 XX CE Human prostate expression marker cDNA J8422.
 XX KW Human prostate cancer, cytostatic, carcinogen, pharmacodynamic marker;
 KW Pharmacogenomic marker, gene; ss.
 XX OS Homo sapiens.
 XX PN W0200150860-A2.
 XX PD 23 AUG-2001.
 XX PF 20-FEB-2001; 2001WG-US05171.
 XX PR 17-FEB-2001; 2000US-183319P.
 XX PP 16-MAR-2000; 2000US-189862P.
 XX PP 25-MAY-2000; 2000US-207454P.
 XX PP 09-JUN-2000; 2000US-211314P.
 XX PP 18-JUL-2000; 2000US-219007P.
 XX PP 13-DEC-2000; 2000US-255281P.

(MILLI-) MILLENNIUM PREDICTIVE MEDICINE INC.

PI Schlegel R, Endege WO, Monahan JE;

DR WPI: 2001-662795/76.

XX Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer.

PS Claim 1: Page 5930-5931; 11750pp; English.

XX The invention relates to an isolated nucleic acid molecule (1) comprising a nucleotide sequence given in tables 1-9 (ARV00010-ARV62213) of the specification or its complement. (1) is useful for:

CC (a) assessing whether a patient is afflicted with prostate cancer;

CC (b) monitoring the progression of prostate cancer in a patient;

CC (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;

CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;

CC (e) selecting a composition for inhibiting prostate cancer in a patient;

CC (f) assessing the prostate cell carcinogenic potential of a compound;

CC (g) determining whether prostate cancer has metastasized in a patient;

CC (h) assessing the aggressiveness or indolence of prostate cancer in a patient;

CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker.

XX Sequence 3645 BP: 1041 A: 793 C: 684 G: 1119 T: 8 other:

Alignment Scores:

Prod. No.: 5,360-139 Length: 3645
 Score: 1431.00 Matches: 262
 Percent Similarity: 93.92% Conservative: 16
 Best Local Similarity: 88.51% Mismatches: 14
 Query Match: 91.32% Indels: 4
 DB: 23 Gaps: 1

US-09-624-670-63 (1-292) x ABV28431 (1-3645)

QY 1 MetGluGluIleuLeuValAspAcnGluValAcpAlaPheLeuAspAsnMetPheGly 20
 DB 85 AUGCAACATCAAGGCTTTCATGATGATCAAAATCAATGCTTTTGGCAATATGTTGGA 144
 QY 21 ProArgSerArgValArgGlyTyrPheLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 40
 DB 145 GGGGAGATTCTGAGTCAGAGTGCTTACGTTGGACTTCTTACCTTCTACCTTTT 204
 QY 41 LeuThrIleThrPheLeuLeuSerIleThrPheLeuLeuLeuLeuLeuLeuLeuLeuLeu 60
 DB 205 CTTACTGTCATGATGATGCTTCAATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 264
 QY 61 AlaLeuSerLeuArgGlyIleLeuThrLeuTyrAsnLeuAlaIleThrLeuLeuSerAla 80
 DB 245 GCTCTTCT 124
 QY 81 TyrMetLeuValGluLeuIleLeuSerSerIlePheGlyGlyIleTyrAsnLeuGlnCysGln 100
 DB 425 TACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 484
 QY 101 AsnLeuAspSerAlaGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 120
 DB 485 GATCTTACACGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 444
 QY 121 PheSerLysLeuValGluIlePheLeuAspThrIlePhePheValLeuArgLysLysThrAsn 140
 DB 445 TTTCTCAAAAC 504
 QY 141 GluIleThrPheLeuHisValTyrHisHisAlaSerMetPheAsnIleThrPheCysVal 160
 DB 505 CAGATTACTTTCTGATGATATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 564
 QY 161 LeuAsnTrpIlePheCysCysGlyClnSerPheGlyProIleLeuAsnSerPheIleHis 180
 DB 565 TTTCAACATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 624
 QY 181 IleLeuMetTyrSerTyrGlyLeuSerValPheProSerMetHisTyrLeuTrp 200
 DB 625 ATCTTATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 684
 QY 201 TrpLysLysTyrLeuThrGluAlaGluLeuValGlnPheValLeuThrIleThrHisThr 220
 DB 685 TGGAGAAATATCTCAACAGCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 744
 QY 221 LeuSerAlaValValLysProGlyPheProIleGlyCysLeuIlePheGlnSerSer 240
 DB 745 ATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 804
 QY 241 TyrMetMetThrLeuValIleLeuPheLeuAspPheTyrIleGlnThrThrArgAlaLysLys 260
 DB 805 TATAGCTAAAGTATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 864
 QY 261 ProValLysGlyGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 276
 DB 865 CCAATGAAGAAATATCTCAACAGCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 924
 QY 277 TysAlaHisSerIleValAlaAsnGlyMetIleAspLysLysAlaGln 292
 DB 925 AAAGCTTACTTCAATGAGGAAAAGGAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 972
 RESULT 6
 ABK46370
 ID ABK46370 standard: cDNA: 900 bp.
 XX AC ABK46370;
 XX DT 05 JUN 2002 (first entry)
 XX DE Mouse elongase MBL01 cDNA.
 XX KW sst; gene; elongase; polyunsaturated fatty acid; puta; transgenic plant;
 KW transgenic non-human animal; plant oil; arachidonic acid; nutritional;
 KW pharmaceutical; cosmetic; animal feed; testostosis; angioplasty; AIDS;

KW as isolated, immunodeficiency syndrome; multiple sclerosis; cachexia; asthma;
 KW inflammatory skin diseases; osteoporosis; kidney stone; cancer; psoriasis;
 KW inflammation; rheumatoid arthritis; psoriasis; platelet aggregation;
 XX vasodilation; cholesterol reduction; gastrointestinal bleeding.
 OS Mus sp.
 XX W0200208401-AZ.
 XX 41-JAN 2002.
 XX 24-JUL-2001: 2001W0-US-2259.
 XX 24-JUL-2000: 2000US-0624670.
 XX 11-JUL 2001: 2001US 0903456.
 XX (ABNO) ABNO11 LAB.
 XX Mukerji P, Das T, Huang Y, Parker Barnes JM, Leonard AF,
 P1 Thurmond J, Pereira SL,
 XX WPI: 2002 172011/22.
 DB P-PSDH: AA087844.
 XX Isolated nucleic acid sequences encoding elongase proteins, useful in
 PT the production of polyunsaturated fatty acids, e.g. arachidonic acid,
 PT which can then be used as nutritional compositions and pharmaceutical
 PT compositions (for treating AIDS).
 XX Claim 8; Fig 58; 27pp; English.
 CC The invention relates to isolated nucleic acid sequences encoding
 CC elongase proteins and the elongase proteins themselves. Also
 CC included are a purified polypeptide which encodes polyunsaturated
 CC fatty acids and has at least 30% amino acid similarity to the amino acid
 CC sequence to an elongase protein, a vector comprising the nucleic
 CC acid, a plant cell (or tissue or whole plant) comprising the vector and
 CC expressing the nucleic acid, a plant oil or acid expressed by the
 CC transgenic plant, and a transgenic non-human animal expressing elongase
 CC in its fluid, the nucleic acids and elongase proteins may be used
 CC directly or indirectly in the production of polyunsaturated fatty acids
 CC (puta), for e.g. arachidonic acid, which can then be used as nutritional
 CC compositions, pharmaceutical compositions, cosmetics and animal feeds.
 CC The pharmaceutical compositions may be used in the treatment of
 CC restenosis after angioplasty, AIDS (acquired immunodeficiency syndrome),
 CC multiple sclerosis, inflammatory skin diseases, osteoporosis, kidney or
 CC urinary tract stones, malignant cancer, cachexia associated with cancer,
 CC eczema, symptoms of inflammation, rheumatoid arthritis, asthma and
 CC psoriasis. They are also useful for inhibiting platelet aggregation,
 CC inducing vasodilation, reducing cholesterol, reducing or preventing
 CC gastrointestinal bleeding and side effects of non-steroidal
 CC anti-inflammatory drugs. The present sequence encodes an elongase
 CC of the invention.

XX Sequence 900 bp: 209 A: 256 G: 200 G: 245 T: 6 other:

Alignment Scores:

Prod. No.: 2,686 90 Length: 900
 Score: 956.50 Matches: 108
 Percent Similarity: 71.58% Conservative: 46
 Best Local Similarity: 58.95% Mismatches: 76
 Query Match: 61.04% Indels: 4
 DB: 24 Gaps: 1

US 09 624 670-63 (1 292) x ABK46370 (1-900)

QY 4 LeuLysAlaPheAspAsnGluValAsnAlaPheLeuLeuAsnMetPheArgAsp 24
 DB 1 ATGCAATATTCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 108
 QY 24 SerArgValArgGlyTyrPheLeuLeuAspSerTyrIleGlnThrPheLeuThrIle 44
 DB 61 ACAAAGATCAAGGCAAGTTCCTCCCTGGCAAAATTAATATGCTTACGTTGCTGCTGCTGCT 120

QY 44 ThrTyrLeuLeuSerIleTrrPheGlyAsnLysTyrMetLysAspArgProAlaLeuSer 63
 Db 121 ATTACTTAA-T-ATTATATG-TGGAA-TAAATAA-ATAAACA-AGG-AGG-TT-T-AT 180
 QY 64 LeuArgGlyIleLeuLeuLeuLeuLeuAlaIleThrLeuLeuSerAlaTyrMetLeu 83
 Db 181 TGGCAGCAGTGTGATTTATTAACCTTGGACATCACTGCTGCTGCTCTACTCATCTTC 240
 QY 84 ValGluLeuIleLeuSerSerTrpGluGlyTyrAsnLeuGlnCysGlnAsnLeuAsp 103
 Db 241 TATGACGTGGTGCACAGGCTGTGGCAGGCGCAAAATACAACTTTCTGCGCAACACGC 300
 QY 104 SerAlaGlyGluGlyAspValArgValAlaLysValLeuTrrPrrTrrPrrPheSerLys 123
 Db 301 AGCGGGAGAAAGAAATATTAAGATATCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
 QY 124 LeuValGluPheLeuAspThrIlePhePheValLeuArgLysLysThrAsnGlnIleThr 143
 Db 361 CTCATCGAATTCACACACCTTTCTTCATCTCCCAAGACCAACACCATCACC 420
 QY 144 PheLeuHisValTyrHisHisAlaSerMetPheAsnIleTrrPrrCysValLeuAsnTrp 163
 Db 421 GTCCTCCATCTTACACACACCTACCATGCTCAACATCTGCTGCTGCTGCTGCTGCTGCTG 480
 QY 164 TrpProCysGlyCysLeuSerPhePheGlyProThrLeuAsnSerPheIleHisIleLeuMet 183
 Db 481 GLLVAVTGGAAATATATATTTTATGAGAGAACTAAAGTTCATCATCTGCTGCTGCTGCTG 540
 QY 184 TyrSerTyrTyrGlyLeuSerValPheProSerMetHisLysTyrLeuTrrPrrPrrLys 203
 Db 541 TACTGTATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
 QY 204 TyrLeuThrGlyAlaGlnLeuValGlnPheValLeuThrIleThrHisThrLeuSerAla 223
 Db 601 TATATCACTAAAGAAATATGAGAGAACTAAAGTTCATCATCTGCTGCTGCTGCTGCTGCTG 660
 QY 224 ValValLysProCysGlyThrIleGlyCysLeuIlePheGlnSerSerTyrMetMet 243
 Db 661 GTT-TT 720
 QY 244 ThrLeuValIleLeuPheLeuAspPheTyrIleGlnThrTyrArgLysLysProValLys 263
 Db 721 TCCCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
 QY 264 LysGluLeuGlnGluLysValLysAsnGlyPheProLysAlaHisLeuIleValAla 283
 Db 781 CGG-----AGCAAGACACCTGAAGCGGCCACCAAGCGGCTGCTGCTGCTGCTGCTGCTG 841
 QY 284 AsnGlyMetThrAsp 288
 Db 842 AAGGACACACCAAC 846
 RESULT 7
 ID ABV23421 standard; cDNA; 2001 BP.
 AC ABV23421;
 DT 16-SEP-2002 (first entry)
 DE Human prostate expression marker cDNA 23412.
 KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
 KW pharmacodynamic marker; gene; ss
 OS Homo sapiens.
 FN W0200160860-A2.
 PD 23-AUG-2001.
 PF 20-FEB-2001; 2001W0-US05171

XX 17 FIB 2000; 2000US-183319P.
 PP 16-MAP-2000; 2000US-18962P.
 PP 25 MAY 2000; 2000US-207454P.
 PP 09 JUN 2000; 2000US-211414P.
 PP 18 JUL 2000; 2000US-219007P.
 PP 13 DEC 2000; 2000US-255281P.
 XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 PA Schlegel R, Endege WO, Monahan JE;
 XX WPI; 2001-662795/76.
 DR
 XX Novel isolated nucleic acid molecule associated with cancerous state of
 PT prostate cells and correlating with presence of prostate cancer, useful
 PT for detecting presence of prostate cancer, stage of prostate cancer -
 US Claim 1; Page 4265-4266; 11750pp; English.
 CC The invention relates to an isolated nucleic acid molecule (I) comprising
 CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV2213) of the
 CC specification or its complement (I) is useful for:
 CC (a) assessing whether a patient is afflicted with prostate cancer;
 CC (b) monitoring the progression of prostate cancer in a patient;
 CC (c) assessing the efficacy of a test compound to inhibit prostate
 CC cancer in a patient;
 CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
 CC in a patient;
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;
 CC (f) assessing the prostate cell carcinogenic potential of a compound;
 CC (g) determining whether prostate cancer has metastasized in a patient;
 CC (h) assessing the aggressiveness or indolence of prostate cancer in a
 CC patient;
 CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.
 XX Sequence 2001 BP; 527 A; 581 C; 399 G; 489 T; 5 other,
 SQ

Alignment Scores
 Pred No Length: 2001
 Score: 951.50 Matches: 167
 Percent Similarity: 72.83% Conservative: 42
 Best Local Similarity: 58.19% Mismatches: 73
 Query Match: 60.72% Indels: 5
 DB: 23 Gaps: 2

US-09-624-670-63 (1-292) x ABV23421 (1-2001)
 QY 3 GlnLeuLysAlaPheAspAsnGluValAsnAlaPheLeuAspAsnMetPheGlyProArg 22
 Db 174 CAATGGACATTTTGGATGATCATCACTTAGTACCTATTTCAGGCAATTCAGGCGCTCGA 233
 QY 23 AspSerArgValArgGlyTrpPheLeuLeuAspSerTyrLeuProThrPheIleLeuThr 42
 Db 234 GATACCTAGAGTAAAGAGGATGGTTCTTCTTCTGACAAATATATACCCACATTTATCTGCT 293
 QY 43 IleThrTyrLeuLeuSerIleTrrPrrLysLysLysTyrMetLysAsnArgProAlaLeu 62
 Db 294 GTCATATATTACTAAATGATGGTGGGACCAAAACATAGAGATAAAACCCATTC 353
 QY 63 SerLeuArgGlyIleLeuThrLeuTyrAsnLeuAlaIleThrLeuLeuSerAlaTyrMet 82
 Db 354 TTTGAGAGGATTTTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 413
 QY 83 LeuValGluLeuLeuSerSerTrpGluGlyTyrAsnLeuGlnCysGlnAsnLeu 102
 Db 414 TTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 473
 QY 103 AspSerAlaGlyGluGlyAspValArgValAlaLysValLeuTrrPrrTrrPrrPheSer 122
 Db 474 CGCAGCGCAGGAGATCAGATATGAAGATTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 533
 QY 123 LysLeuValGluPheLeuAspThrIlePhePheValLeuArgLysLysThrAsnGlnIle 142

DB 534 AAACATCATGAATTTATGAGACACTTCTTCCTTCATCTGCGCAAGAACACACACAGATC 593
 QY 143 ThrPheLeuHisValTyrHisHisAlaSerMetPheAsnIleThrPyrCysValLeuAsp 362
 DB 594 AGGCTGCTGCAGCTACACCATGCGCTGATGCTGAATATCTGGTGGTTTGTGATGAAC 653
 QY 163 TrpIleProTyrGlyGluSerPhePheGlyProThrLeuAsnSerPheIleHisIleLeu 182
 DB 654 TGGGCGCTCGCGGCACCTCTATTTTGGTGGCCACACTTAATPACTTCAACACGTCCTC 713
 QY 184 MetTyrSerTyrTyrGlyLeuSerValPhePheSerMetHisLysTyrIleuTrpTrpLys 202
 DB 714 ATGTACTCTTACTATGTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 773
 QY 203 LysTyrLeuThrGlnAlaGlnLeuValGlnPheValLeuThrIleThrHisThrLeuSer 222
 DB 774 AAGTACATCACTCAGGAGACACTGCTTCACTTTGTGTGACAAATCATCCAGACCTGCTC 833
 QY 224 AlaValValLysProTyrGlyPhePheProPheGlyCysLeuIlePheGlnSerSerTyrMet 242
 DB 834 GGGGCAICATGGCGGCGPACATGCCCTCTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTG 893
 QY 244 MetThrLeuValIleLeuPheLeuAspPheTyrIleLeuThrTyrArgLysLysProVal 262
 DB 894 ATTGCGTGAATGCTGCTTCTTCAAACTTCAATTCATCAAGCTCAACAAAGAGAGGGGGC 953
 QY 263 LysGlyGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 281
 DB 954 TCGGAG 1001
 QY 282 ValAlaAsnGlyMetThrAsp 288
 DB 1002 GCTGTGAATGGACACACAGAG 1022
 RESULT 8
 ABV24778
 ID ABV24778 standard: cDNA; 2001 BP.
 AC ABV24778;
 DT 16-SEP-2002 (first entry)
 DE Human prostate expression marker cDNA 24769.
 KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
 KW pharmacogenomic marker; gene; ss
 OS Homo sapiens.
 PN W0200160860 A2.
 PD 24 AUG-2001.
 PF 20 FEB-2001; 2001W010505171
 PR 17 FEB-2000; 2000US 184319P.
 PR 16 MAR 2000; 2000US 189862P.
 PR 25 MAY-2000; 2000US 207454P.
 PR 09-JUN 2000; 2000US 21134P.
 PR 18-JUL-2000; 2000US 219097P.
 PR 14 DEC-2000; 2000US 255281P.
 PA (MILL.) MILLENNIUM PREVENTIVE MEDICINE INC.
 XX Schlegel R, Endege WJ, Monahan JE;
 XX WPI; 2001-662795/76.
 XX Novel isolated nucleic acid molecule associated with cancerous state of
 XX prostate cells and correlating with presence of prostate cancer, useful
 XX for detecting presence of prostate cancer, stage of prostate cancer -
 XX

PS Claim 1; Page 4740-4741; 11750pp; English.
 XX The invention relates to an isolated nucleic acid molecule (1) comprising
 CC a nucleotide sequence given in Tables 1-5 (ABV24778-ABV24783) of the
 CC specification or its complement. (1) is useful for:
 CC (a) assessing whether a patient is afflicted with prostate cancer;
 CC (b) monitoring the progression of prostate cancer in a patient;
 CC (c) assessing the efficacy of a test compound to inhibit prostate
 CC cancer in a patient;
 CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
 CC in a patient;
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;
 CC (f) assessing the prostate cell carcinogenic potential of a compound;
 CC (g) determining whether prostate cancer has metastasized in a patient;
 CC (h) assessing the aggressiveness or indolence of prostate cancer in a
 CC patient;
 CC (1) is also useful as a pharmacodynamic or pharmacogenomic marker.
 XX Sequence 2001 BP; 527 A; 581 C; 399 G; 489 T; 5 other;

Alignment Scores:
 Prod. No.: 2,650-89 Length: 2001
 Score: 951.50 Matches: 167
 Percent Similarity: 72.82% Conservations: 42
 Best Local Similarity: 58.19% Mismatches: 74
 Query Match: 69.72% Indels: 1
 DB: 23 Gaps: 2

US 09-624-670-63 (1 292) x ABV24778 (1 2001)
 QY 3 GlnLeuLysAlaPheAspAsnGluValAsuAlaPheLeuAspAsuMetPheGlyProArg 22
 DB 174 CAATGGCAACATTTGATGCAATCCTTACCTGATGCTGCTGCTGCTGCTGCTGCTGCTG 233
 QY 23 AspSerArgValArgClyTrpPheLeuLeuAspSerTyrLeuProThrIleLeuLeuThr 42
 DB 234 GATACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 293
 QY 43 IleThrTyrLeuLeuSerIleThrPheGlyAsnLysTyrMetLysAsnArgProAlaLeu 62
 DB 294 GTCAATATTTTACATTTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 353
 QY 63 SerLeuArgGlyIleLeuThrLeuTyrAsnLeuAlaIleThrIleLeuSerAlaTyrMet 82
 DB 454 TCT 413
 QY 83 LeuValGlnLeuIleLeuSerSerTyrGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 102
 DB 414 TTCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 473
 QY 103 AspSerAlaGlyGlyIleValArgValAlaValLysValLeuThrPyrTrpTrpPheSer 122
 DB 474 GGCACGCGAGCAGAAATCAGATATGAGATATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 533
 QY 123 CysLeuValGlnPheLeuAspThrIlePhePheValLeuArgLysLysThrAsnGlnIleP 142
 DB 534 AAACATATAGAAATTAAGCAGACCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 593
 QY 143 ThrPheLeuHisValTyrHisHisAlaSerMetPheAsnIleThrPyrCysValLeuAsn 162
 DB 594 AGGCTGCTGCAGCTACACCATGCGCTGATGCTGAATATCTGGTGGTTTGTGATGAAC 653
 QY 163 TrpIleProTyrGlyGluSerPhePheGlyProThrLeuAsnSerPheIleHisIleLeu 182
 DB 654 TGGGCGCTCGCGGCACCTCTATTTTGGTGGCCACACTTAATPACTTCAACACGTCCTC 713
 QY 184 MetTyrSerTyrTyrGlyLeuSerValPhePheSerMetHisLysTyrIleuTrpTrpLys 202
 DB 714 ATGTACTCTTACTATGTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 773
 QY 203 LysTyrLeuThrGlnAlaGlnLeuValGlnPheValLeuThrIleThrHisThrLeuSer 222
 DB 774 AAGTACATCACTCAGGAGACACTGCTTCACTTTGTGTGACAAATCATCCAGACCTGCTC 833

OY	223	AlaValValIysThrCysGlyPheThrPheGlyCysLeuLcPheCAsSerSeryMet	242
Dd	834	GAGPAPATGGGAGGAAATTGGTCTTGTTGTGTTTATTTCACATTGATAATG	893
OY	243	MetThrLeuValIleLeuPheLeuAsnPhetTlLeGluThrTyTAGlyLysProVal	262
Dd	894	AFTTCCTCATTCCTCTCTCCAAAACITCTACATTCAGACTCAACAAGAAGCGGCC	953
OY	263	LysLysGluLeuGlnGlu---LysGluValLysAsnGlyPheProLysAlaHisLeuIle	281
Dd	954	ICCCGAATGAAAAATCAATCTGGAAGGACACACAAAGGC-----TCCATGGCT	1001
OY	282	ValAlaAsnGlyMetThrAsp	288
Dd	1002	GTCTGTGAATGGAACAAACAAAC	1022
RESULT 9			
ABV25364			
ID	ABV25364	standard; cDNA; 2001 BP.	
XX	AC	ABV25364;	
XX	AC		
XX	DT	16-SEP-2002 (first entry)	
XX	XT	Human prostate expression marker cDNA 25355.	
DE	XX		
KW	KW	Human; prostate cancer; cytosolic; carcinogen; pharmacodynamic marker;	
KW	KW	pharmacogenic marker; gene; ss.	
OS	OS	Homo sapiens.	
XX	WO	2000150860-A2	
XX	PN		
XX	PD	23-ACG 2001.	
XX	PP	20-FEB-2001; 2001WO-US05171.	
XX	PP	17-FEB-2000; 2000US-183319P.	
PP	PP	16-MAR-2000; 2000US-189852P.	
PP	PP	25-MAY-2000; 2000US-207454E.	
PP	PP	09-JUN-2000; 2000US-211314P.	
PP	PP	18-JUL-2000; 2000US-219007P.	
PP	PP	13-DEC-2000; 2000US-255281P.	
XX	(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.		
PA	Schlegel R, Endege WO, Monahan JE;		
XX	WPI; 2001-662795/76		
PPT	Novel isolated nucleic acid molecule associated with cancerous state of		
PPT	prostate cells and correlating with presence of prostate cancer, useful		
PPT	for detecting presence of prostate cancer, stage of prostate cancer -		
XX	Claim 1; Page 5005-5006; 11750pp; English.		
XX	The invention relates to an isolated nucleic acid molecule (I) comprising		
CC	a nucleotide sequence given in Tables 1-9 (ASVs009 ASv6213) of the		
CC	specification or its complement. (I) is useful for:		
CC	(a) assessing whether a patient is afflicted with prostate cancer,		
CC	(b) monitoring the progression of prostate cancer in a patient;		
CC	(c) assessing the efficacy of a test compound to inhibit prostate		
CC	cancer in a patient;		
CC	(d) assessing the efficacy of a therapy for inhibiting prostate cancer		
CC	in a patient;		
CC	(e) selecting a composition for inhibiting prostate cancer in a patient;		
CC	(f) assessing the prostate cell carcinogenic potential of a compound;		
CC	(g) determining whether prostate cancer has metastasized in a patient;		
CC	(h) assessing the aggressiveness or indolence of prostate cancer in a		
CC	patient;		
XX	(I) is also useful as a pharmacodynamic or pharmacogenomic marker.		

[illegible]

CC such as leukaemia, lymphoma and neuroblastoma, autoimmune disorders such
 CC as multiple sclerosis, connective tissue disease, rheumatoid arthritis,
 CC diabetes mellitus, allergic rhinitis, asthma and eczema, nervous system
 CC disorders such as Parkinson's disease, Alzheimer's disease, Huntington's
 CC chorea, amyotrophic lateral sclerosis, spinal muscular atrophy and
 CC Wernicke disease, inflammatory disorders such as nephritis, Crohn's
 CC disease, ischaemia reperfusion injury, shock, sepsis and inflammatory
 CC bowel disease. The sequences exhibit activity relating to angiogenesis,
 CC cell proliferation, cell differentiation, stem cell growth factor,
 CC activin or inhibin. Therefore, they can be used to manipulate stem cells
 CC in culture to give rise to neuroepithelial cells that can be used to
 CC augment or replace cells damaged by illness, accidental damage or genetic
 CC disorders. The sequences may also be used for regeneration of bone,
 CC cartilage, tendons and ligaments and in tissue repair and burn healing.
 CC Note: Some sequences for this patent did not form part of the printed
 CC specification, but were obtained in electronic format directly from WIPO
 CC at http://wipo.int/pub/published_pat_sequences.

xx Sequence 2769 BP; 799 A; 543 C; 554 G; 873 T; 0 other;

Alignment Scores:

Field No.:	4,13e-89	Length:	2769
Score:	951.50	Matches:	167
Percent Similarity:	72.82%	Conservative:	42
Host Local Similarity:	58.19%	Mismatches:	73
Query Match:	60.72%	Indels:	5
DB:	22	Gaps:	2

US-09-624-670-63 (1-292) x AAS44747 (1-2769)

QY	3	GlnLeuLysAlaPheAspGluValAlaAsnAlaPheLeuAspAsnMetPheGlyProArg	22
DB	133	CAAAATGGACATTTTATGATCATCATCTAGTACTATTTCAAGACATCTAGGCCCCGCA	192
QY	23	AspSerArgValArgGlyTrpPheLeuLeuAspSerTrpLeuProThrPheIleLeuThr	42
DB	193	GATCTAGAGTAAACCGATCGTTCTCTCGCAGCAATTATATACCCACATTTATCTGCTCT	252
QY	43	IleThrTrpLeuLeuSerIleTrpLeuGlyAsnLysTrpMetLysAsnArgProAlaLeu	62
DB	253	GTCAATATTTTATTAATTTATGATGGTGGGACCAAAATATCATGAGGAATAAACACCATTC	312
QY	63	SerLeuArgGlyIleLeuThrTrpAsnLeuAlaIleThrLeuLeuSerAlaTrpMet	82
DB	313	TCTTGAGAGGAGGATTTTATGATGATATAAAATTGAGATCATCTCTCTCTGTATATG	372
QY	83	LeuValGluLeuLeuLeuSerTrpGlyGlyTrpAsnLeuGlnGlyGlnAsnLeu	102
DB	373	TTCGTCGACATTAAGAAATAGATATGAGGAAAGGCAAAATATCTCTCTCTCTCTCTCT	432
QY	103	AspSerAlaGlyTrpGlyAspValArgValAlaLysValLeuTrpTrpTrpTrpPheSer	122
DB	433	CGTACGGAAGAAAT	492
QY	123	LysLeuValGluPheLeuAspThrIleIlePheValLeuArgLysLysThrAsnGlnIle	142
DB	493	AAACTCATGAAATTAAGAAATATATATATATATATATATATATATATATATATATAT	552
QY	143	ThrPheLeuHisValTrpIleHisAlaSerMetPheAsnIleTrpTrpCysValLeuAsn	162
DB	553	ACGGTCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	612
QY	163	TrpIleProCysGlyGlnSerPheGlyProThrLeuAsnSerPheIleHisIleLeu	182
DB	613	TGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	672
QY	183	MetTrpSerTrpTrpGlyLeuSerValPheProSerMetHisLysTrpLeuTrpTrpLys	202
DB	673	ATGATATTTAT	732
QY	203	LysTrpLeuThrGlnAlaLeuValGlnPheValIleThrIleThrHisLeuSer	222
DB	733	AAGTACATACATCAGGAGGATGATGATGATGATGATGATGATGATGATGATGATGAT	792

QY	223	AlaValValLysProCysGlyPheProPheGlyCysLeuIlePheGlnSerSerTrpMet	242
DB	793	CGGATCACTGCGCGCGACATTCCTCTCTGTTGGTTGTTATTCAGATTGATCATG	852
QY	243	MetThrLeuValIleLeuPheLeuAsnPheTrpIleGlnThrTrpTrpArgLysLysProVal	262
DB	853	ATTCCT	912
QY	263	LysLysGluLeuGlnGlu---LysGluValLysAsnGlyPheProLysAlaHisLeuIle	281
DB	913	TCCCGAAGCAAGACCATCTCAAGCACCACCAAGATGG-----TCCATGGCT	960
QY	282	ValAlaAsnGlyMetThrAsp	288
DB	961	GTTGTGATGAGACACACCAAC	981

RESULT 14

AAS44919
 ID AAS44919 standard; DNA; 3083 BP.

AC AAS44919;

XX 18-DEC-2001 (first entry)

DE Human contig polynucleotide sequence #172.

XX Mammal; human; rhesus monkey; baker's yeast; fission yeast; Norway rat;
 KW mouse; Chinese hamster, African clawed frog; fruit fly; dog; leukaemia;
 KW cancer; lymphoma; neuroblastoma; autoimmune disorder; cell proliferation;
 KW nervous system disorder; inflammatory disorder; cell differentiation; ds;
 KW angiogenesis; stem cell growth factor; activin; inhibin; cartilage; burn;
 KW genetic disorder; bone regeneration; tendon; ligament; tissue repair;
 KW cytotoxic; antirheumatic; antiarthritic; vulnery; antinflammatory;
 KW cytobacterial; immunosuppressive; vasotropic; antiparkinsonian;
 KW neuroprotective; osteopathic; antidiabetic; antiaesthetic; antiallergic;
 KW immunostimulant; analgesic; gene therapy.

XX Homo sapiens.

OS Synthetic.

XX WO200164834-A2.

PN 07-SEP-2001.

XX 26-FEB-2001: 2001WO-0504926.

XX 28-FEB-2000: 2000US-0515126.

XX 18-MAY-2000: 2000US-0577409.

XX 17-JUN-2000: 2000US-0597707.

XX 14-JUL-2000: 2000US-0615807.

XX 19-SEP-2000: 2000US-0664641.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren P;

XX Xue AJ, Yang Y, Wehrman T, Wang J, Ma Y, Wang D, Chen R, Xu C;

XX Drmabac R;

XX WPI: 2001-589862/66.

XX p-PSNR; AAS28019.

XX Novel polypeptides and nucleic acids obtained from cDNA libraries

XX prepared from various human tissues, for diagnosis, treatment of

XX cancer, neurological, inflammatory disorders and for use in arrays for

XX detection -

XX Claim 1: SEQ ID No 516; 153pp; English.

XX Sequences AAS44576-AAS44919 represent full-length polynucleotides and

XX contig polynucleotides encoding polypeptides of the invention. The DNA

XX and protein sequences are useful for the treatment, diagnosis and

XX prevention of various types of disorder in a mammalian subject such as a

CC human, dog, monkey, mouse, hamster or rat. The disorders include cancers
 CC such as leukemia, lymphoma and neuroblastoma, autoimmune disorders such
 CC as multiple sclerosis, connective tissue disease, rheumatoid arthritis,
 CC diabetes mellitus, allergic rhinitis, asthma and eczema, nervous system
 CC disorders such as Parkinson's disease, Alzheimer's disease, Huntington's
 CC chorea, amyotrophic lateral sclerosis, spinal muscular atrophy and
 CC wernicke disease, inflammatory disorders such as nephritis, Crohn's
 CC disease, ischemia reperfusion injury, shock, sepsis and inflammatory
 CC bowel disease. The sequences exhibit activity relating to angiogenesis,
 CC cell proliferation, cell differentiation, stem cell growth factor,
 CC activin or inhibin. Therefore, they can be used to manipulate stem cells
 CC in culture to give rise to neuroepithelial cells that can be used to
 CC augment or replace cells damaged by illness, accidental damage or genetic
 CC disorders. The sequences may also be used for regeneration of bone,
 CC cartilage, tendons and ligaments and in tissue repair and burn healing.
 CC Note: Some sequences for this patent did not form part of the printed
 CC specification, but were obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pat_sequences.

XX
 SU Sequence 3083 BP: 884 A: 594 C: 607 G: 996 I: 2 other:

Alignment Scores:

Prod. No.: 4.79e B9 Length: 3083
 Score: 951.50 Matches: 167
 Percent Similarity: 72.82% Conservative: 42
 Best Local Similarity: 58.19% Mismatches: 73
 Query Match: 63.72% Indels: 5
 DB: 22 Gaps: 2

US 09-624-670-63 (1 242) X AAS44919 (1-3083)

QY 4 GlnLeuValAspAspAsnValAsnAlaPheLeuAspAsnMetPheGlyProArg 42
 DB 134 CAATAGAACATTATTGATGATATCTAGTATGATTTAAAGCATTTGATGCTGCA 192
 QY 23 AspSerArgValArgGlyTrpPheLeuLeuAspSerTrpLeuProthrpPheLeuThr 42
 DB 193 CAIACAGAGAAAGAGATGTTCTCGCAATTAATACCCACATTTATCTGCTCT 252
 QY 4 ThrThrValLeuLeuSerThrTrpLeuGlyValAsnGlySerMetLysAsnArgProAlaLeu 62
 DB 253 GTCATATATTTACTAAATGATGCTGGGACCAAAATACATGAGAAATACACAGCCATTC 312
 QY 64 SerLeuArgGlyTrpLeuThrLeuTrpAsnLeuAlaIleThrLeuLeuSerAlaTrpMet 82
 DB 413 TCTTGGCGGGGATTTTAGTGGTGATATAAGCTTGGACTCACTGCTGCTGTATATG 372
 QY 84 LeuValGlnGlnGlnGlnSerTrpLeuGlyCysTrpAsnLeuGlyCysGlnAsnLeu 102
 DB 374 TCTGTGACCTTAGTAAAGAGACTAAGGAGGAGCAAAATACATGAGAAATACACAGCCATTC 432
 QY 104 AspSerAlaTrpGlyTrpValArgValAlaValAlaValLeuTrpTrpTrpTrpPheSer 122
 DB 434 CGCATCGGACGACAAATACATGAGAAATACATGAGAAATACATGAGAAATACATGAGAAAT 492
 QY 124 CysLeuValGlnPheLeuAspThrTrpPheThrValLeuAlaLysLysThrAsnGlnIle 142
 DB 493 AAATCATAGATTTATGAGACATTTCTTTATGCTGCGTAAGAACACACACACATTC 552
 QY 143 ThrPheLeuHisValTrpHisHisAlaSerMetPheAsnIleTrpTrpValLeuAsn 162
 DB 553 ACCGGCCCGGACGATACATGAGCTGAGTGAACATCTGGTGGTGTGATGATGAC 612
 QY 164 TrpLeuProGlyGlyHisSerPhePheGlyProThrLeuAsnSerPheLeuHisIleLeu 182
 DB 613 TGGGCGCCGCGGACGATGATTTATTTGGTGGCAGACATTAATAGCTTCATCCACGCGCC 672
 QY 184 MetTrpSerTrpTrpGlyLeuSerValProPheSerMetHisLysLysLysTrpTrpPhe 202
 DB 674 ATGACTCTTATGATGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 732
 QY 204 LysTrpLeuPheLeuValLeuValLeuValLeuValLeuValLeuValLeuValLeuVal 222

DB 733 AAGTAAATACACTACAGGCGAGCTCTTTCAGTTCTCTTTCAGTAAATACACTACACTCT 792
 QY 223 AlaValValLysTrpCysGlyPheTrpPheGlyGlyLeuLeuPheLeuSerTrpMet 242
 DB 794 GAGGTCATCTGGAGGAGCATATTCAGCTCTTGGATGGATGGATTCAGATGATATG 852
 QY 243 MetThrLeuValIleLeuPheLeuAspPheTrpIleIleIleThrTrpArgLysLysProVal 262
 DB 853 ATTTCGCTGATGCTCTCTTCACCAATTTCTACATTAGACCTACACACAGAAAGGCGGC 912
 QY 263 LysLysGlnLeuGlnGluLeuLysGlnValLysAsnGlyPheProLysAlaHisLeuIle 281
 DB 913 TCCGCAAGAAAGAAATATATCTCAAGATATATCAAAATGAGGAGGAGGAGGAGG 960
 QY 282 ValAlaAsnGlyMetThrAsp 288
 DB 961 GCTGTGATGACACACACCAAC 981
 RESULT 15
 AAA54132
 ID AAA54132 standard; DNA: 2710 bp.
 XX
 AC AAA54132;
 XX
 DI 08 FEB-2001 (first entry)
 XX
 DE Breast cancer protein BCR2 coding sequence
 XX
 KW Breast cancer; diagnosis; prognosis; detection; screening;
 KW antibody; estrogen receptor; anti-estrogen; immune response;
 KW lymph node; metastases; tumour; BCR1; BCR2; BCR3; BCR4; BCR5; BCR6; BCR7;
 XX BCR8; BCR9; BCR10; BCR11; BCR12; BCR13; BCR14; BCR15; BCR16; BCR17; BCR18; BCR19; BCR20; BCR21; BCR22; BCR23; BCR24; BCR25; BCR26; BCR27; BCR28; BCR29; BCR30; BCR31; BCR32; BCR33; BCR34; BCR35; BCR36; BCR37; BCR38; BCR39; BCR40; BCR41; BCR42; BCR43; BCR44; BCR45; BCR46; BCR47; BCR48; BCR49; BCR50; BCR51; BCR52; BCR53; BCR54; BCR55; BCR56; BCR57; BCR58; BCR59; BCR60; BCR61; BCR62; BCR63; BCR64; BCR65; BCR66; BCR67; BCR68; BCR69; BCR70; BCR71; BCR72; BCR73; BCR74; BCR75; BCR76; BCR77; BCR78; BCR79; BCR80; BCR81; BCR82; BCR83; BCR84; BCR85; BCR86; BCR87; BCR88; BCR89; BCR90; BCR91; BCR92; BCR93; BCR94; BCR95; BCR96; BCR97; BCR98; BCR99; BCR100; BCR101; BCR102; BCR103; BCR104; BCR105; BCR106; BCR107; BCR108; BCR109; BCR110; BCR111; BCR112; BCR113; BCR114; BCR115; BCR116; BCR117; BCR118; BCR119; BCR120; BCR121; BCR122; BCR123; BCR124; BCR125; BCR126; BCR127; BCR128; BCR129; BCR130; BCR131; BCR132; BCR133; BCR134; BCR135; BCR136; BCR137; BCR138; BCR139; BCR140; BCR141; BCR142; BCR143; BCR144; BCR145; BCR146; BCR147; BCR148; BCR149; BCR150; BCR151; BCR152; BCR153; BCR154; BCR155; BCR156; BCR157; BCR158; BCR159; BCR160; BCR161; BCR162; BCR163; BCR164; BCR165; BCR166; BCR167; BCR168; BCR169; BCR170; BCR171; BCR172; BCR173; BCR174; BCR175; BCR176; BCR177; BCR178; BCR179; BCR180; BCR181; BCR182; BCR183; BCR184; BCR185; BCR186; BCR187; BCR188; BCR189; BCR190; BCR191; BCR192; BCR193; BCR194; BCR195; BCR196; BCR197; BCR198; BCR199; BCR200; BCR201; BCR202; BCR203; BCR204; BCR205; BCR206; BCR207; BCR208; BCR209; BCR210; BCR211; BCR212; BCR213; BCR214; BCR215; BCR216; BCR217; BCR218; BCR219; BCR220; BCR221; BCR222; BCR223; BCR224; BCR225; BCR226; BCR227; BCR228; BCR229; BCR230; BCR231; BCR232; BCR233; BCR234; BCR235; BCR236; BCR237; BCR238; BCR239; BCR240; BCR241; BCR242; BCR243; BCR244; BCR245; BCR246; BCR247; BCR248; BCR249; BCR250; BCR251; BCR252; BCR253; BCR254; BCR255; BCR256; BCR257; BCR258; BCR259; BCR260; BCR261; BCR262; BCR263; BCR264; BCR265; BCR266; BCR267; BCR268; BCR269; 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? EARLIER FILING DATE: 1997-06-06
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? EARLIER FILING DATE: 1997-10-02

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RESULT 2
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? GENERAL INFORMATION:
? APPLICANT: Rosen et al.
? TITLE OF INVENTION: 186 Human Secreted proteins
? FILE REFERENCE: P2002PL
? CURRENT APPLICATION NUMBER: US/09/149,476
? EARLIER FILING DATE: 1998-09-08
? EARLIER APPLICATION NUMBER: PCT/US98/04493
? EARLIER FILING DATE: 1998-03-06
? EARLIER APPLICATION NUMBER: 60/040,162
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49	EARLIER FILING DATE: 1997-08-22	
50	EARLIER APPLICATION NUMBER: 60/056, 610	
51	EARLIER FILING DATE: 1997-08-22	
52	EARLIER APPLICATION NUMBER: 60/056, 878	
53	EARLIER FILING DATE: 1997-08-22	
54	EARLIER APPLICATION NUMBER: 60/056, 662	
55	EARLIER FILING DATE: 1997-08-22	
56	EARLIER APPLICATION NUMBER: 60/056, 872	
57	EARLIER FILING DATE: 1997-08-22	
58	EARLIER APPLICATION NUMBER: 60/056, 892	
59	EARLIER FILING DATE: 1997-08-22	
60	EARLIER APPLICATION NUMBER: 60/056, 637	
61	EARLIER FILING DATE: 1997-08-22	
62	EARLIER APPLICATION NUMBER: 60/056, 903	
63	EARLIER FILING DATE: 1997-08-22	
64	EARLIER APPLICATION NUMBER: 60/056, 888	
65	EARLIER FILING DATE: 1997-08-22	
66	EARLIER APPLICATION NUMBER: 60/056, 879	
67	EARLIER FILING DATE: 1997-08-22	
68	EARLIER APPLICATION NUMBER: 60/056, 880	
69	EARLIER FILING DATE: 1997-08-22	
70	EARLIER APPLICATION NUMBER: 60/056, 894	
71	EARLIER FILING DATE: 1997-08-22	
72	EARLIER APPLICATION NUMBER: 60/056, 911	
73	EARLIER FILING DATE: 1997-08-22	
74	EARLIER APPLICATION NUMBER: 60/056, 610	
75	EARLIER FILING DATE: 1997-06-13	
76	EARLIER APPLICATION NUMBER: 60/061, 060	
77	EARLIER FILING DATE: 1997-08-22	
78	EARLIER APPLICATION NUMBER: 60/056, 874	
79	EARLIER FILING DATE: 1997-08-22	
80	EARLIER APPLICATION NUMBER: 60/056, 910	
81	EARLIER FILING DATE: 1997-08-22	
82	EARLIER APPLICATION NUMBER: 60/056, 884	
83	EARLIER FILING DATE: 1997-08-22	
84	EARLIER APPLICATION NUMBER: 60/056, 631	
85	EARLIER FILING DATE: 1997-08-22	
86	EARLIER APPLICATION NUMBER: 60/056, 845	
87	EARLIER FILING DATE: 1997-08-22	
88	EARLIER APPLICATION NUMBER: 60/056, 892	
89	EARLIER FILING DATE: 1997-08-22	
90	EARLIER APPLICATION NUMBER: 60/057, 761	
91	EARLIER FILING DATE: 1997-08-22	
92	EARLIER APPLICATION NUMBER: 60/047, 595	
93	EARLIER FILING DATE: 1997-05-23	
94	EARLIER APPLICATION NUMBER: 60/047, 599	
95	EARLIER FILING DATE: 1997-05-23	
96	EARLIER APPLICATION NUMBER: 60/047, 568	
97	EARLIER FILING DATE: 1997-05-23	
98	EARLIER APPLICATION NUMBER: 60/047, 585	
99	EARLIER FILING DATE: 1997-05-23	
100	EARLIER APPLICATION NUMBER: 60/047, 586	
101	EARLIER FILING DATE: 1997-05-23	
102	EARLIER APPLICATION NUMBER: 60/047, 590	
103	EARLIER FILING DATE: 1997-05-23	
104	EARLIER APPLICATION NUMBER: 60/047, 594	
105	EARLIER FILING DATE: 1997-05-23</	

234 CysLeuIlePheGlnSerSerTyMetMetThrLeuValIleLeuPheLeuAspPheTyr 253
1447 TGGGCGCATTTT---TCTTCATATTTG-----GTACTATTATTATTCATTAC 1491
254 ILeGlnThrTyrArgLysLysProValLysLysGluLeuGlnGluLysGluValLysAsn 273
1492 ATTAACGTTTATTAAGCTAAAGGACCAACCAAGCAGTAGAGTGTAAAGCGGTGCGGACGGC 1551
274 G1Y 274
1552 GGT 1554
D3
RESULT 5
US-09-145-828A-1
Sequence 1, Application US/09145828A
Patent No. 6403349
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Mukerji, Pradip
APPLICANT: Leonard, Amanda E. Y.
APPLICANT: Huang, Yung-Sheng
APPLICANT: Thurmond, Jennifer
APPLICANT: Kitchen, Stephen J.
APPLICANT: Parker-Barnes, Jennifer M.
TITLE OF INVENTION: THE ELONGASE GENE AND USES THEREOF
FILE REFERENCE: 6407.1S.01
CURRENT APPLICATION NUMBER: US/09/145,828A
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 954
TYPE: DNA
ORGANISM: Mortierella alpina
US-09-145-828A-1
Alignment Scores:
Pred. No.: 1 Re-23 Length: 254
Score: 279.00 Matches: 89
Percent Similarity: 42.99% Conservative: 55
Best Local Similarity: 26.57% Mismatches: 107
Query Match: 17.80% Indels: 84
Gaps: 13
US-09-624-670-63 (1-292) x US-09-145-828A-1 (1-954)
QY 9 AsnGluValAsnAlaPheLeuAspAsnMetPheGlyProArgAspSerArgValArgLys 28
Db 19 GACAAGGTCAAGCTCGCATTTGATGACCTTCGGAATCAAG----- 60
QY 29 TrpPheLeuAspSerTyr-----Leu 36
Db 61 -----CTGACAGCTACTTCTTGTAAAGTATGAATTTTAACTGGAAGTCCATC 111
QY 37 ProPhePheLeu----- 41
Db 112 GACTCTCTGCTCTTCCAGAGAGGATGATGATGATGATGATGATGATGATGATGATGATGAT 171
QY 42 ---ThrIleThrTyrLeuLeuSerIleTyrPheGlyAsnLysTyrMetLysAsnArgPro 60
Db 172 TGGACTATCACTACTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 231
QY 61 AlaLeuSerLeuArgGlyIleLeuThrIleTyrAsnLeuAlaIlePheIleLeuSerAla 80
Db 232 GCGCTTCAAGTCAAGTCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 291
QY 81 TyrIleLeuValGluLeuIle-----LeuSerSerTyrPheGlyLysTyr 95
Db 292 TCGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 351
QY 96 AsnLeuGlnLysGlnAsnLeuAspSerAlaGlyGluGlyAspValArgValAlaLysVal 115

Db 352 TAGCATATTGAGAGAT-----GAGTATGATGATGATGATGATGATGATGATGATGATGAT 399
QY 116 LeuIleTyrPheTyrPheSerTyrLeuValIlePheLeuAspPheIlePhePheValLeu 135
Db 400 TACTACTTAAATTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 459
QY 136 ArgLysLysThrAsnGlnIleThrPheLeuHisValIleHisHisAlaSerMetPheAsn 155
Db 460 AAGATTAAT-----CTCTTACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 513
QY 156 IleTyrPhePheValLeu-----AsnTyrIleProGlyCysIleSer 169
Db 514 CTCTGTTTCTTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 564
QY 170 PhePheGlyProThrLeuAsnSerPheIleHisIleLeuMetTyrSerTyrTyrGlyLeu 189
Db 565 -----AACCCAACTTCACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 612
QY 190 SerValPheProSerMetHisLysTyrLeuTyrPhePheLysTyrLeuGluAlaGln 209
Db 613 TCT-----GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 663
QY 210 LeuValIlePheValLeuThrIle-----ThrHisThrLeuSerAla 223
Db 664 ATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 723
QY 224 Val-----ValLysProGlyCysIlePheProPheCysLys 235
Db 724 TTGACATTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 783
QY 236 ILePheGlnSerSerTyrMetMetThrLeuValIleLeuPheLeuAspPheTyrIleGln 255
Db 784 CTCTTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 843
QY 256 ThrTyrArgLysLysProValLysLysLysLysLysLysLysLysLysLysLysLysLys 275
Db 844 ACCTAAAT-----GATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 894
QY 276 TrpLysAlaHisIleCysIleValAlaAsnGlyMetCysAspArgLys 290
Db 895 CCGCAAGCT-----CTCAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 940
RESULT 6
US-09-145-828A-9
Sequence 9, Application US/09145828A
Patent No. 6403349
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Mukerji, Pradip
APPLICANT: Leonard, Amanda E. Y.
APPLICANT: Huang, Yung-Sheng
APPLICANT: Thurmond, Jennifer
APPLICANT: Kitchen, Stephen J.
APPLICANT: Parker-Barnes, Jennifer M.
TITLE OF INVENTION: THE ELONGASE GENE AND USES THEREOF
FILE REFERENCE: 6407.1S.01
CURRENT APPLICATION NUMBER: US/09/145,828A
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 9
LENGTH: 587
TYPE: DNA
ORGANISM: Mortierella alpina
US-09-145-828A-9
Alignment Scores:
Pred. No.: 1 29e-18 Length: 587
Score: 235.00 Matches: 42
Percent Similarity: 48.04% Conservative: 36
Best Local Similarity: 30.39% Mismatches: 68
Query Match: 15.00% Indels: 38
Gaps: 7

Page 11

US-08-298-829-7	Alignment Scores:	Score:	Length:	989
US-08-298-829-7	2,42e-13	193.00	Matches:	55
		44.554	Conservative:	35
		27.234	Mismatches:	58
		12.324	Indels:	54
			Gaps:	10
US-08-624-670-6 (1-294) x US-08-298-829-7 (1-989)				
QY	115	ValLeuTrpTrp-----	-TyrTyrPheSerTysLeuValGluPheLeuAspThrIle	1311
Db	907	CTCTTTTCTGGGGCATATATCTTCCTACCTCTCCCAAGATTTGTAATATATGAAATGCTT	948	
QY	132	PhePheValLeuAlaGlyLysThrAsnGlnIleThrPheLeuHisValTyrHisHisAla	1515	
Db	847	TTTCATCATCCTCAGCCGATACATACAAACAGCAGTACCTTCCCTTCCAGTACACATAC	768	
QY	152	SeuMetPheAsnIleTrpTrpCysValLeuAsnTrpIleProCysGlnGlnSerPhePhe	1711	
Db	787	AT	737	
QY	172	GlyProThrLeu-----	AsnSerPheIleHisIleGlnMetTyrSerTyrTyrGlyLeu	189
Db	736	CGCAT	677	
QY	190	SeuValPheProSerMetHisLysTyrLeuTrpTrpTyrLysTyrLeuThrGlnAlaGln	209	
Db	676	TGCACCCCTC-----CGGATATGACCCCAAG-----	626	
QY	210	LeuValGluPhe-----	ValLeuTrpIleThrHisThrLeu	221
Db	625	CTGGTAT	566	
QY	222	SeuAlaValValLysProCysGlyPheProPheCysLys-----	236	
Db	565	GCTCTC-----	533	
QY	237	PheGlnSerSerTyrMetMetThrLeuValIleLeuPheLeuAsnProTyrIleGlnThr	256	
Db	532	TTTCATATGAGGCTTACAGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	473	
QY	257	TyrArgLysLysProValLysLysGluLeuGlnGlyLysGluValLysAsn-----	273	
Db	472	TAC-----	434	
QY	274	-----	-GlyPheProLysAlaHisGlnLeuVal	282
Db	433	TTAT	374	
QY	283	AlaAsn	264	
Db	373	GTTTCA	368	
RESULT 12				
US-08-787-335-6/c				
Sequence 6, Application US/08787335				
Patent No. 5981834				
GENERAL INFORMATION:				
APPLICANT: John, Mattyaka E.				
APPLICANT: Umbeck, Paul F.				
APPLICANT: Brill, Winston J.				
TITLE OF INVENTION: GENETICALLY ENGINEERED COTTON PLANTS				
NUMBER OF SEQUENCES: 18				
CORRESPONDENCE ADDRESS:				
ADDRESS: Quares and Brady				
STREET: P O Box 2113				
CITY: MADISON				
STATE: WISCONSIN				

COMPUTER: U.S.A
ZIP: 54701
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 4.50 inch, 800KB storage
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft Word 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/787 335
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/540,797
FILING DATE:
APPLICATION NUMBER: US/07/253,243
FILING DATE: 04-OCT-89
ATTORNEY/AGENT INFORMATION:
NAME: Nicholas J. Sosa
REGISTRATION NUMBER: 27,486
REFERENCE/DOCKET NUMBER: 1122990245
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 989 base pairs
TYPE: nucleic acid
STRANDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYDROTHERMAL: no
ANTI SENSE: no
ORIGINAL SOURCE:
ORGANISM: Gossypium hirsutum
STRAIN: Toker 412
DEVELOPMENTAL STAGE: 10 day old fiber cells
TISSUE TYPE: fiber cells
IMMEDIATE SOURCE:
LIBRARY: CREF10
CLONE: All
US 08 787 335 6

Alignment Scores:
Pred. No.: 2 42e 13
Score: 194.00 Length: 989
Percent Similarity: 44.55% Matches: 55
Host local Similarity: 27.23% Conserved: 35
Query Match: 12.42% Mismatch: 58
DB: 2 Indels: 54
caps: 10

US 09 624-670 63 (1 292) x US 08 787 335 6 (1 989)

QY 115 ValGluThrPp TYTYRPhgSerLysGluValGluPhgGluAspThrLeu 131
DB 907 GTCTTTTGGGATAATCTCTATGCTCTCAACATTTTAATTATGACACCCCTT 848
QY 132 PheGluValGluAspGlySerThrAsnGlnIleGlnPheGluHisValTyrHisHisAla 151
DB 847 TGTGATATGCTGATGATCAAGCAAGCAATACCTGCTGACGCTGATGATGATGCTG 788
QY 152 SerMetPheAsnIleTyrTyrPheValLeuAsnTyrIleProGlySerTyrHisSerPhePhe 171
DB 787 ATGCTGATCAATGATGATTAATATGCTTAAAGAC AGCTGCTAGCTGCTGCTA 737
QY 172 GlyProThrLeu AsnSerPheIleHisIleLeuMetTyrSerTyrTyrGlyLeu 189
DB 736 GCTATGCTGTGATGCAAGCAAGCTGCTGATGCTGATGCTGATGCTGATGCTGCTG 677
QY 190 SerValPheProSerMetHisLysTyrLeuTyrPheGlySerTyrGluGlnAlaGln 209
DB 676 TGCACCTCTGAGGATACAGCTCAAGACACAGCAAGCAAGCAAGCAAGCAAGCAAG 626
QY 210 LeuValGluThrPp ValGluThrIleThrHisThrLeu 221
DB 625 GTGCTGATGATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 566

QY 222 SerAlaValValLysSerGlySerPheThrGlyGlyGly 246
DB 565 GCTCTT ----- GATGCTTTGGGATTTGATTTGCTT 543
QY 237 PheIleSerSerTyrMetMetTyrLeuValIleLeuHisGluAsnPheTyrIleSerThr 256
DB 532 TTTATGATGACGTCACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 473
QY 257 TyrMetTyrSerProValIleLeuGlyGlyLeuGluGluGluHisValValGlyAla 273
DB 472 TAC-----TTCACCAATGCTAAGGTTTAAAGGTTAACTAAATA 434
QY 274 -----GlyPheThrGlyAlaHisSerIleVal 282
DB 433 TTAATTAACCAATTTTTTTTTTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTT 474
QY 283 AlaAsn 284
DB 473 GCTTCA 368

RESULT 13
US-09-149-476-259
Sequence 259 Application us/09/149476
Patent No. 6420526
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: P2002P1
CURRENT APPLICATION NUMBER: US/09/149,476
EARLIER FILING DATE: 1998-09-08
EARLIER APPLICATION NUMBER: P01/00598/04493
EARLIER FILING DATE: 1998-04-06
EARLIER APPLICATION NUMBER: 60/040,162
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,333
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/038,621
EARLIER FILING DATE: 1997-04-07
EARLIER APPLICATION NUMBER: 60/040,626
EARLIER FILING DATE: 1997-04-07
EARLIER APPLICATION NUMBER: 60/040,384
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,386
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,163
EARLIER FILING DATE: 1997-04-07
EARLIER APPLICATION NUMBER: 60/047,600
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,615
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,597
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,502
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,633
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,583
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,617
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,618
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,503
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,592
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,581
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,584
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,500
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,587

Mon Jun 16 09:01:12 2003

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Page 13

EARLIER FILING DATE: 1997-05-23	EARLIER APPLICATION NUMBER: 60/047,442
EARLIER FILING DATE: 1997-05-23	EARLIER APPLICATION NUMBER: 60/047,588
EARLIER FILING DATE: 1997-05-23	EARLIER APPLICATION NUMBER: 60/047,613
EARLIER FILING DATE: 1997-05-23	EARLIER APPLICATION NUMBER: 60/047,582
EARLIER FILING DATE: 1997-05-23	EARLIER APPLICATION NUMBER: 60/047,596
EARLIER FILING DATE: 1997-05-23	EARLIER APPLICATION NUMBER: 60/047,612
EARLIER FILING DATE: 1997-05-23	EARLIER APPLICATION NUMBER: 60/047,632
EARLIER FILING DATE: 1997-05-23	EARLIER APPLICATION NUMBER: 60/047,601
EARLIER FILING DATE: 1997-05-23	EARLIER APPLICATION NUMBER: 60/043,580
EARLIER FILING DATE: 1997-04-11	EARLIER APPLICATION NUMBER: 60/043,568
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EARLIER FILING DATE: 1997-04-11	EARLIER APPLICATION NUMBER: 60/043,311
EARLIER FILING DATE: 1997-04-11	EARLIER APPLICATION NUMBER: 60/043,671
EARLIER FILING DATE: 1997-04-11	EARLIER APPLICATION NUMBER: 60/043,674
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EARLIER FILING DATE: 1997-04-11	EARLIER APPLICATION NUMBER: 60/043,312
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EARLIER FILING DATE: 1997-04-11	EARLIER APPLICATION NUMBER: 60/043,672
EARLIER FILING DATE: 1997-04-11	EARLIER APPLICATION NUMBER: 60/043,315
EARLIER FILING DATE: 1997-04-11	EARLIER APPLICATION NUMBER: 60/048,974
EARLIER FILING DATE: 1997-06-06	EARLIER APPLICATION NUMBER: 60/056,886
EARLIER FILING DATE: 1997-08-22	EARLIER APPLICATION NUMBER: 60/056,877
EARLIER FILING DATE: 1997-08-22	EARLIER APPLICATION NUMBER: 60/056,880
EARLIER FILING DATE: 1997-08-22	EARLIER APPLICATION NUMBER: 60/056,893
EARLIER FILING DATE: 1997-08-22	EARLIER APPLICATION NUMBER: 60/056,630
EARLIER FILING DATE: 1997-08-22	EARLIER APPLICATION NUMBER: 60/056,878
EARLIER FILING DATE: 1997-08-22	EARLIER APPLICATION NUMBER: 60/056,662
EARLIER FILING DATE: 1997-08-22	EARLIER APPLICATION NUMBER: 60/056,872
EARLIER FILING DATE: 1997-08-22	EARLIER APPLICATION NUMBER: 60/056,882
EARLIER FILING DATE: 1997-08-22	EARLIER APPLICATION NUMBER: 60/056,637
EARLIER FILING DATE: 1997-08-22	EARLIER APPLICATION NUMBER: 60/056,903
EARLIER FILING DATE: 1997-08-22	EARLIER APPLICATION NUMBER: 60/056,888
EARLIER FILING DATE: 1997-08-22	EARLIER APPLICATION NUMBER: 60/056,879
EARLIER FILING DATE: 1997-08-22	EARLIER APPLICATION NUMBER: 60/056,880
EARLIER FILING DATE: 1997-08-22	EARLIER APPLICATION NUMBER: 60/056,894
EARLIER FILING DATE: 1997-08-22	EARLIER APPLICATION NUMBER: 60/047,610

EARLIER FILING DATE: 1997 06 13
 EARLIER APPLICATION NUMBER: 60/061,060
 EARLIER FILING DATE: 1997 10 02

Alignment Scores:

Prod. No.: 2,790 06 Length: 814
 Score: 132.00 Matches: 32
 Percent Similarity: 51.92% Conservative: 22
 Best Local Similarity: 40.17% Mismatches: 46
 Query Match: 8.42% Indels: 4
 DB: 4 Gaps: 3

US-09-624-670-63 (1 292) x US-09-149-476-259 (1 814)

QY 2 GluAlaLeuValAspAlaPheAspGluValAlaAlaPheLeuAspAsnMetPheGlyPro 21
 DB 14 GATCTCTTACGCGAGATGAGAGCTGTGTGCACTTGTATCAAGAGGTGATG---AGGTAC 90
 QY 22 ArGAspSerAvalArGAlaGlyTTPheLeuLeuAspSer TyrLeuProThrPhe 49
 DB 91 GCAATATCCGAGATGAGAGCTGCTGCTGATGAGTGGTGGCTGGTAATGAGCTGCATT 150
 QY 40 TLeuThrTLeuThrTLeuLeuSerTLeuTTPheGlyValuLeuGlyTyrMetLysAsnArg 59
 DB 151 CTCTGACCTACGCTGATCTCTT---CTCTGACTGGGCTGCAATCAAGCTTAATGCT 207
 QY 60 PheAlaLeuSerLeuAlaGlyTLeuGlyThrLeuTyrAsnLeuAlaTLeuLeuLeuSer 79
 DB 208 AACGCTTCGCTGATCTGCTGCTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 267
 QY 80 AlaTyrMetLeuValTLeuLeuLeuLeuSerSerTTPheGlyGlyTyrAsnLeuGlyLys 99
 DB 248 CTCTGATCTGATCTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 327
 QY 100 GluAsnLeuAsp 163
 DB 328 GATCTCTACGAG 349

RESULT 14

US-09-172-108-45
 Sequence 45, Application US/09122108
 Patent No. 6160104
 GENERAL INFORMATION:
 APPLICANT: Cundigham, Mary Jane
 APPLICANT: Panzer, Gary B.
 APPLICANT: Selthamer, Jeffrey J.
 TITLE OF INVENTION: MARKERS FOR PROXIMAL PROLIFERATORS
 FILE REFERENCE: PA-0012 US
 CURRENT APPLICATION NUMBER: US/09/172-108
 CURRENT FILING DATE: 1998 10 14
 NUMBER OF SEQ ID NOS: 56
 SOFTWARE: PERL Program
 SEQ ID NO 45
 LENGTH: 124
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: unsure
 LOCATION: 34, 53, 87, 109, 122
 OTHER INFORMATION: a of g or c or t, unknown, or other
 FEATURE:
 OTHER INFORMATION: 700545965411
 US-09-172-108-45

Alignment Scores:

Prod. No.: 3,16 06 Length: 124
 Score: 121.00 Matches: 25
 Percent Similarity: 66.67% Conservative: 1
 Best Local Similarity: 64.10% Mismatches: 12
 Query Match: 7.72% Indels: 1
 DB: 4 Gaps: 0

US-09-624-670-63 (1 292) x US-09-172-108-45 (1 124)

QY 198 TyrLeuTTPheGlyTTPheThrGluAlaThrLeuValuLeuThrValuLeuThrVal 217
 DB 4 TACTCTGGGAGGAGAGAGATGATCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 62
 QY 217 CTThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThr 249
 DB 63 CATCAACAGCAGAGCTGGGAGGATCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 117

RESULT 15

US-08-417-330A-15
 Sequence 15, Application US/08417330A
 Patent No. 5719057
 GENERAL INFORMATION:

APPLICANT: BADENHUM, KAREN
 APPLICANT: LE FOUQUELLES, BEATRICE
 APPLICANT: WHITTING, PAUL
 APPLICANT: WINGROVE, PETER
 TITLE OF INVENTION: STABLE TRANSFECTED CELL LINE EXPRESSING
 TITLE OF INVENTION: GABA-A RECEPTOR AND NOVEL CLONED
 TITLE OF INVENTION: GABA-A RECEPTOR SUBUNIT cDNA SEQUENCES
 NUMBER OF SEQUENCES: 20
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: J. MARK HAND - MEROX & CO., INC.
 STREET: 126 EAST LINCOLN AVENUE P.O. BOX 2000
 CITY: RAYWAY
 STATE: NJ
 COUNTRY: US
 ZIP: 07065-0900
 COMPUTER READABLE FORM:
 MEDIUM TYPE: diskette
 COMPUTER: IBM compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/417, 330A
 FILING DATE: 05-Apr-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: HAND, MARK
 REGISTRATION NUMBER: 46,545
 REFERENCE/WORK NUMBER: 711091A
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 908-594-3905
 TELEFAX: 908-594-4720
 INDEX:
 INFORMATION FOR SEQ ID NO: 15:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2310 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: Coding Sequence
 LOCATION: 298...1683
 OTHER INFORMATION:
 US-08-417-330A-15

Alignment Scores:

Prod. No.: 0,074 Length: 2410
 Score: 100.00 Matches: 59
 Percent Similarity: 35.00% Conservative: 53
 Best Local Similarity: 18.44% Mismatches: 108
 Query Match: 6.38% Indels: 101
 DB: 1 Gaps: 11

US-09-624-670-63 (1 292) x US-08-417-330A-15 (1 2410)

Mon Jun 16 09:01:12 2003

us-09-624-670-63.rn1

Page 15

QY 28 G1YTPPhleuLeuAspSerTyrLeuProThrPheIleuThrIleThrTyrLeuLeu 47
DE 1069 GAGTACTTTGTCATCCACACCTTACCTTCCCTGGCATATGACCTGATCTTATCATCAGGTG 1128
QY 48 SerIleThrLeuGlyAsnLysTyrMetLysAsnArgProAlaLeuSerLeuArgIle 67
DE 1129 TCCTTTGGCTGACACCGCAATCATCAGCCAGACACTTTTGGCTGACACCGGTG 1188
QY 68 LeuThrLeuTyrAsnLeuAlaIleThrLeuLeuSerAlaTyrMetLeuValGluLeu 87
DE 1189 CTGACCATGACGACCTGACATCATCAGCCAGCAACTCTGCCCCAAGTGGCTAGGCC 1248
QY 88 LeuSer---SerThrProLugIyGlyTyrAsnLeuGlnCysGlyAsnLeuAspSerAlaGly 106
DE 1249 ACCGCCATGACCTGG----- 1263
QY 107 GluGlyAspValArgValAlaLysValLeuThrPrtPrtTyrTyrPheSerLysLeuValGlu 126
DE 1264 -----TTTCATACCTGTGTCTATGCTTGTCTGCGCCGTGATAG 1308
QY 127 PheLeuAspThrIlePhePhe----- 133
DE 1309 TTGCGCAGGTCATTTACTTTACCAAGAGAGCTGGCCGTGAGATGCCAATAAGCCTTG 1368
QY 134 -----ValLeuArgLysTyrAsnGlnIle 142
DE 1369 GAGGAGCCAGATCAGAAAAAGCGTGAAGTCATCTAATTAATGCAATCAAGCCTTT 1428
CY 143 ThrPheLeuHisValTyrHisHisAlaSerMetPheAsnIleThrPrtPrtCysValLeuAsn 162
DE 1429 ACAACTGGAGAGATGTCTCCACCCCAAC----- 1458
QY 163 TrpIleProCysGlyGlnSerPhePheGlyProThrLeuAsnSerPheIleHisIle--- 181
DE 1459 --ATTCCGACGAAACAGACCCGAGGAGCGTCGAAATACACCTCAGCTCAGATAAA 1515
QY 182 -----LeuMetTyrSerTyrTyrGlyLeuSer----- 190
DE 1516 CCCTTGAAAGACACTTCTGAAGAGCAAAAAAGACTTACAAACATGATCAGCPAAATGAC 1575
QY 191 -----ValPheProSerMet-----HisLysTyrLeuThrPrtPrtLys 202
DE 1576 AAAATGTCCGAAATGTATTCACACTGTGTGCGCACTTTCACAACTTAACTTAACTGCGCA 1635
QY 203 LysTyrLeuThrGlnAlaGlnLeuValGlnPhe----- 213
DE 1636 ACGTATTGCAATGAGCGCGGTGATAAAGG-AGCGGCTCTCCAAAATATACGGGCGCAC 1694
QY 214 -----ValLeuThrIleThrHisThrLeuSerAlaValAlaLysProCysGlyPhe--- 230
DE 1695 ACTCCCAAACTCCAGACAGACATCTCCAGCAAAATGTACCCAGAGAGAGAGGTTTGGCT 1754
QY 231 -----ProPheGlyCysLeuIlePheGlnSerTyrMetLeuThrLeuVal 246
DE 1755 CACAGGCACTCTCCATATGACACACTTTCAGCAAAATTTTGCATGTTAATATATA 1814
QY 247 -----IleLeuPheLeuAsnPheTyr-IleGlnThrTyrArgLysLys 260
DE 1815 TGTACAAATATATATGCTTGATGTTTCTA--TATGTAACCTTCAGATGTTTCCAAAGATG 1871
QY 260 sProValLysLysGluLeuGlnGluLysGluValLysAsnGlyPheProLysAlaHis 279
DE 1872 TCCCATGTATATTCGCAACAACTTCTGAAAAACAGATAGATGACTGACAC 1929

Search completed: June 15, 2003, 23:43:20
Job time : 61.3604 secs



GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OW protein - nucleic search, using frame-1/us-f2a model

Run on: June 15, 2003, 23 02 06 Search time 127 966 seconds
(without alignments) 3304.262 Million cell updates/sec

Tfile: US-09-624-670-63

Perfect score: 1567
Sequence: 1 MEOLKAFDEYNATLIONNEG.....NGEPKAIH IVANMTTKKAQ 292

Scoring table: RI/SUM62

Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 1029858 seqs, 724030393 residues

Total number of hits satisfying the search parameters: 2059716

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Command line parameters: -db=us-1p
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-LOOPCT=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blowsum62
-TRANS-human40.cdi -LIST=45 -DOCALLIGN=200 -THR_SCORE=prt -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTPMT=ptc -NORM=ext -HNPSTGTP=500 -MINLEN=0
-MATH=2000000000 -USPR=US096246702CON_11_102.stunat_11062003_075433_11745
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-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database: Published Applications NA:

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2. /cgn2.6/ptodata/1/pubpna/PC1_NEW_PUB.seq.*
3. /cgn2.6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
4. /cgn2.6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
5. /cgn2.6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
6. /cgn2.6/ptodata/1/pubpna/PC1US_PUBCOMB.seq.*
7. /cgn2.6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
8. /cgn2.6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
9. /cgn2.6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
10. /cgn2.6/ptodata/1/pubpna/US09_PUBCOMB.seq.*
11. /cgn2.6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
12. /cgn2.6/ptodata/1/pubpna/US10_PUBCOMB.seq.*
13. /cgn2.6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
14. /cgn2.6/ptodata/1/pubpna/US06_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1567	100.0	879	9	US-09-849-199A-22
2	1567	100.0	879	10	US-09-903-456-5
3	1431	91.3	2426	9	US-10-198-846-13406
4	956	61.0	900	10	US-09-903-456-6

5	941.5	60.1	914	10	US-09-903-456-4	Sequence 3, Appl
6	749	47.8	748	9	US-09-764-868-352	Sequence 352, App
7	670.5	42.8	871	9	US-09-764-868-353	Sequence 353, App
8	462.5	29.5	1492	9	US-09-809-391-258	Sequence 258, App
9	462.5	29.5	1542	9	US-09-809-391-106	Sequence 106, App
10	420.5	26.8	1682	10	US-09-822-830A-145	Sequence 145, App
11	403.5	25.7	819	10	US-09-903-456-7	Sequence 7, Appl
12	403.5	25.7	819	10	US-09-903-456-72	Sequence 72, Appl
13	401.5	25.6	819	10	US-09-903-456-73	Sequence 73, Appl
14	397.5	25.4	819	10	US-09-903-456-74	Sequence 74, Appl
15	397.5	25.4	819	10	US-09-903-456-75	Sequence 75, Appl
16	397.5	25.4	819	10	US-09-903-456-76	Sequence 76, Appl
17	396.5	25.3	818	10	US-09-903-456-77	Sequence 77, Appl
18	394.5	25.2	819	10	US-09-903-456-78	Sequence 78, Appl
19	393.5	25.1	819	10	US-09-903-456-79	Sequence 79, Appl
20	375	23.3	549	9	US-09-903-456-74	Sequence 74, Appl
21	368	23.5	24664	9	US-09-903-456-74	Sequence 74, Appl
22	368	23.5	24664	9	US-09-903-456-74	Sequence 74, Appl
23	348	22.2	430	9	US-09-918-995-17480	Sequence 17480, A
24	329	21.0	384	9	US-09-918-995-37438	Sequence 37438, A
25	306	19.5	630	9	US-09-903-456-67	Sequence 67, Appl
26	305.5	19.4	427	9	US-09-903-456-67	Sequence 67, Appl
27	279	17.8	954	10	US-09-903-456-1	Sequence 1, Appl
28	267	17.0	194	10	US-09-864-761-10025	Sequence 10025, A
29	267	17.0	194	10	US-09-864-761-10025	Sequence 10025, A
30	267	17.0	409	10	US-09-864-761-10025	Sequence 10025, A
31	267	17.0	485	10	US-09-864-761-10025	Sequence 10025, A
32	267	17.0	8861	9	US-09-764-868-1445	Sequence 1445, Ap
33	265	16.9	455	10	US-09-864-761-10025	Sequence 10025, A
34	235	15.0	587	10	US-09-864-761-10025	Sequence 10025, A
35	232	14.8	590	10	US-09-864-761-10025	Sequence 10025, A
36	209	13.3	867	10	US-09-903-456-17	Sequence 17, Appl
37	200.5	12.8	795	9	US-09-903-456-4	Sequence 4, Appl
38	200.5	12.8	798	9	US-09-903-456-63	Sequence 63, Appl
39	200.5	12.8	2775	9	US-10-161-521A-221	Sequence 221, App
40	200.5	12.8	2989	9	US-09-759-130B-231	Sequence 231, App
41	196	12.5	813	9	US-09-759-130B-238	Sequence 238, App
42	161	10.3	2932	9	US-09-759-130B-241	Sequence 241, App
43	160.5	10.2	322	9	US-09-759-130B-242	Sequence 242, App
44	158.5	10.1	511	9	US-09-918-995-10797	Sequence 10797, A
45	155	9.9	167	10	US-09-783-590-46	Sequence 46, Appl

ALIGNMENTS

RESULT 1
US-09-849-199A-22
Sequence 22, Application US/09849199A
Publication No. US29030082754A1
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Mukerji, Pradip
APPLICANT: Thumond, Jennifer M.
APPLICANT: Huang, Yung-Sheng
APPLICANT: Das, Tapas
TITLE OF INVENTION: DELTA 4-THESATPASE GENES AND USES
TITLE OF INVENTION: THEPROF
FILE REFERENCE: 6904 US-01
CURRENT APPLICATION NUMBER: US/09/849,199A
CURRENT FILING DATE: 2002-04-15
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 22
LENGTH: 879
TYPE: DNA
ORGANISM: Mus musculus
US-09-849-199A-22
Alignment Scores:
Prod No: 7 849 169
Score: 1567.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Matches: 879
Mismatch: 0

Query Match: 100.00% Indel: 0
 DB: 9 Gaps: 0
 US-09-624-670-63 (1-292) x US-09-624-197A-22 (1-879)

UY 1 MetGluGlnLeuValAlaPheAspAsnGluValAsnAlaIlePheLeuAspAsnMetPheGly 20
 DB 1 ATGCAAGACCTGGAACCTCTTGGAATGAATGACCAATGCTCTTGGAACCAATGCTTGGA 60
 UY 21 PheAlaGspSerAlaValAlaGlyTTPPheLeuLeuAspSerTyrLeuProThrPheLe 40
 DB 61 CCAAGACATTCGACGCTCTGAGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
 UY 41 LeuThrLeuThrTyrLeuLeuSerLeuTyrPheLeuTyrAsnLeuValAlaIleThrLeuLeuSerAla 80
 DB 121 CTCACATCATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
 UY 61 AlaLeuSerLeuAlaGlyTyrLeuThrLeuTyrAsnLeuValAlaIleThrLeuLeuSerAla 80
 DB 181 GCT 240
 UY 81 TyrMetLeuValGluLeuValLeuLeuSerSerTyrPheLeuTyrTyrAsnLeuGlnCysGln 100
 DB 241 TATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 400
 UY 101 AsnLeuAspSerAlaValGlyLeuTyrAspValAlaValAlaGlyValLeuTyrTyrTyr 120
 DB 401 AATCTGCACACTGATACATGAGGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 460
 UY 121 PheSerTyrLeuValGluLeuLeuAspPheThrLeuThrValLeuThrValLeuThrValLeu 140
 DB 161 TTTCTTAAACTAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
 UY 141 GlnIleThrPheLeuGlnValTyrHisHisAlaSerMetPheAsnIleTyrTyrPheVal 160
 DB 421 CACATGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
 UY 161 LeuAsnTyrPheTyrProTyrGlnSerPhePheGlyProThrLeuAsnSerPheLeuHis 180
 DB 481 TTTGACGCTGATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
 UY 181 PheGlnMetTyrSerTyrTyrGlyLeuSerValPheTyrSerMetHisTyrTyrLeuTyr 200
 DB 541 ATTCTGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
 UY 201 TrrPheTyrTyrLeuThrGlnAlaGlnLeuValGlnPheValLeuThrIleThrHisThr 220
 DB 601 TGCAGAGAGTATCTTAATAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
 UY 221 LeuSerAlaValAlaValGlySerGlyPheThrPheLeuTyrGlySerGlnThrGlnSer 240
 DB 661 CTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
 UY 241 TyrMetMetThrLeuValAlaIlePheLeuAsnPheTyrIleGlnThrTyrArgTyrGly 260
 DB 721 TATAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
 UY 261 ProValTyrLeuSerGlnGlnGlnGlnValAlaGlyAsnGlnPheProTyrAlaHisGln 280
 DB 781 CCACTTACAG 840
 UY 281 LeuValAlaAsnIleMetThrAspTyrGlyAlaGln 292
 DB 841 ATTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 876

RESULT 2

US-09-603-456-5

Sequence 5, Application US-09-603-456

Patent No. US20020138874A1

GENERAL INFORMATION:

APPLICANT: Abbott Laboratories

APPLICANT: Mockett, Pradip

APPLICANT: Leonard, Joon-Young

APPLICANT: Huang, Yung-Sheng
 APPLICANT: Perotica, Suzette L.
 TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF
 FILE REFERENCE: 6407-05-P3
 CURRENT APPLICATION NUMBER: US-09-603-456-5
 CURRENT FILING DATE: 2001-07-11
 PRIOR APPLICATION NUMBER: US-09-624-670
 PRIOR FILING DATE: 2000-07-24
 PRIOR APPLICATION NUMBER: US-09-624-670
 PRIOR FILING DATE: 1999-08-23
 PRIOR APPLICATION NUMBER: US-09-624-670
 PRIOR FILING DATE: 1998-09-02
 NUMBER OF SEQ ID NOS: 116
 SOFTWARE: FASTSEQ for Windows Version 4.0
 SEQ ID NO 5
 TYPE: DNA
 ORGANISM: Mus musculus
 US-09-603-456-5

Alignment Scores:

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Query Match:	100.00%	Mismatches:	0
DB:	10	Indels:	0
		Gaps:	0

US-09-624-670-63 (1-292) x US-09-603-456-5 (1-879)

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 DB 1 ATGCAAGACCTGGAACCTCTTGGAATGAATGACCAATGCTCTTGGAACCAATGCTTGGA 60
 UY 21 PheAlaGspSerAlaValAlaGlyTTPPheLeuLeuAspSerTyrLeuProThrPheLe 40
 DB 61 CCAAGACATTCGACGCTCTGAGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
 UY 41 LeuThrLeuThrTyrLeuLeuSerLeuTyrPheLeuTyrAsnLeuValAlaIleThrLeuLeuSerAla 80
 DB 121 CTCACATCATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
 UY 61 AlaLeuSerLeuAlaGlyTyrLeuThrLeuTyrAsnLeuValAlaIleThrLeuLeuSerAla 80
 DB 181 GCT 240
 UY 81 TyrMetLeuValGluLeuValLeuLeuSerSerTyrPheLeuTyrTyrAsnLeuGlnCysGln 100
 DB 241 TATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 400
 UY 101 AsnLeuAspSerAlaValGlyLeuTyrAspValAlaValAlaGlyValLeuTyrTyrTyr 120
 DB 401 AATCTGCACACTGATACATGAGGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 460
 UY 121 PheSerTyrLeuValGluLeuLeuAspPheThrLeuThrValLeuThrValLeuThrValLeu 140
 DB 161 TTTCTTAAACTAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
 UY 141 GlnIleThrPheLeuGlnValTyrHisHisAlaSerMetPheAsnIleTyrTyrPheVal 160
 DB 421 CACATGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
 UY 161 LeuAsnTyrPheTyrProTyrGlnSerPhePheGlyProThrLeuAsnSerPheLeuHis 180
 DB 481 TTTGACGCTGATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
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 DB 541 ATTCTGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
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Score: 956.5
Percent Similarity: 71.58%
Best Local Similarity: 58.95%
Query Match: 61.04%
DB: 10
Gaps: 1

US 09 624 670 63 (1 292) x US 09 903 456 6 (1 900)

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4 LeuylsAlpheAspAsnGluValAsnAlaPheLeuAspAsnMetPheGlyProAlaAsp 24
1 ATGCAACATTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 60
24 SerAlaValAlaGlyIlePheLeuLeuLeuAspSerIleLeuProIlePheLeuIle 43
61 ACAAACATCAACAGCAACATGCTGCTGACATTAATGCTGATGCTGCTGCTGCTGCT 120
44 ThrIleLeuLeuSerIleIlePheLeuValAsnLysIleLysAsnAlaProAlaLeu 63
121 ATTACTACATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
64 LeuAlaGlyIleLeuIleLeuIleLeuIleLeuIleLeuIleLeuIleLeuIleLeu 83
181 TGCGAGAGCATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
84 ValGluLeuLeuLeuSerIlePheLeuIleGlyIleIleIleIleIleIleIleIle 300
241 TATAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 400
104 SerAlaGlyIleLeuIleLeuIleLeuIleLeuIleLeuIleLeuIleLeuIleLeu 123
101 AGCGAGGACAAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAAT 160
124 LeuValGluLeuLeuLeuIleIlePhePheValLeuAlaLysValLeuIlePheIle 143
361 CTCATGCAATTCATGCAATTCATGCAATTCATGCAATTCATGCAATTCATGCAATTC 420
144 PheLeuIleValIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 163
421 GTGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 480
164 IleProLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 183
481 GTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
184 TyrSerTyrTyrTyrTyrTyrTyrTyrTyrTyrTyrTyrTyrTyrTyrTyrTyrTyr 203
541 TACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
204 TyrLeuIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 223
601 TACATCAATCAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
224 ValValLysProLysGlyPheProIleGlyCysLeuLeuIleGluIleSerSerTyr 243
661 GTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
244 ThrLeuValIleLeuPheLeuAspPheTyrIleGlyThrTyrTyrTyrTyrTyrTyr 263
721 TCGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
264 LysIleLeuLeuIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 283
781 GGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 341
284 AsnGlyMetThrAsp 284
812 AACGACAAACAAACAAAC 816

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RESULT 5

US 09 903 456 6

Sequence 3, Application US/09/03456

Patent No. US2002018874A1

GENERAL INFORMATION

```

APPLICANT: Abbott Laboratories
APPLICANT: Mukerji, Pradip
APPLICANT: Leonard, Amanda Eun-yeon
APPLICANT: Huang, Yung-Sheng
APPLICANT: Pereira, Suzette L.
TITLE OF INVENTION: CLONING GENES AND USING THEREOF
FILE REFERENCE: 6407 US 34
CURRENT APPLICATION NUMBER: US 09/624,670
PRIORITY FILING DATE: 2001 07-11
PRIORITY APPLICATION NUMBER: US 09/624,670
PRIORITY FILING DATE: 2000 07-24
PRIORITY APPLICATION NUMBER: US 09/379,095
PRIORITY FILING DATE: 1999-08-23
PRIORITY APPLICATION NUMBER: US 09/145,828
PRIORITY FILING DATE: 1998-09-02
NUMBER OF SEQ ID NOS: 116
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO: 3
LENGTH: 914
TYPE: DNA
ORGANISM: Homo sapiens
US-09-903-456-3

Alignment Scores:
Prod. No.: 1,456-97 Length: 914
Score: 941.50 Matches: 165
Percent Similarity: 72.73% Conservat: 44
Best Local Similarity: 57.69% Mismatches: 73
Query Match: 60.08% Indels: 5
DB: 10 Gaps: 2

US-09-624 670-63 (1-292) x US-09-903-456-3 (1-914)
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24 SerAlaValAlaGlyIlePheLeuLeuLeuAspSerIleLeuProIlePheLeuIle 43
61 ACAAACATCAACAGCAACATGCTGCTGACATTAATGCTGATGCTGCTGCTGCTGCT 120
64 LeuAlaGlyIleLeuIleLeuIleLeuIleLeuIleLeuIleLeuIleLeuIleLeu 83
121 ATTACTACATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
124 LeuValGluLeuLeuLeuIleIlePhePheValLeuAlaLysValLeuIlePheIle 143
361 CTCATGCAATTCATGCAATTCATGCAATTCATGCAATTCATGCAATTCATGCAATTC 420
144 PheLeuIleValIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 163
421 GTGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 480
164 IleProLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 183
481 GTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
184 TyrSerTyrTyrTyrTyrTyrTyrTyrTyrTyrTyrTyrTyrTyrTyrTyrTyrTyr 203
541 TACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
204 TyrLeuIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 223
601 TACATCAATCAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
224 ValValLysProLysGlyPheProIleGlyCysLeuLeuIleGluIleSerSerTyr 243
661 GTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
244 ThrLeuValIleLeuPheLeuAspPheTyrIleGlyThrTyrTyrTyrTyrTyrTyr 263
721 TCGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
264 LysIleLeuLeuIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 283
781 GGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 341
284 AsnGlyMetThrAsp 284
812 AACGACAAACAAACAAAC 816

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[illegible]

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1 RESULT: 11
2 US 09/903,456.7
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Alignment Scores:	
Period: No.:	2 to 36
Score:	403.98
Percent Similarity:	52.96%
Best Local Similarity:	83.70%
Query Match:	25.74%
DB:	10
	caps:

[illegible]

0Y	AspSerAlaLysIleLysLysAspValGluValAlaLysValLeuThrIleTyrTyrIle	120
0B	322 GAGAGAGGCAACCAACGCTCATGCTTCAGGAGCATGCTGCTCATGCTGCTGCTGCTG	382
0Y	122 SerTyrLeuValGluIleIleIleAspThrIleIleIleValLeuAlaGlyLysThrAspGln	182
0B	382 TCTAAAGATACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	442
0Y	142 IleIleIleIleIleValValTyrHisHisAlaSerMetProAsnIleIleIleIleIleVal	202
0B	442 GTTCTCTCTTCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	502
0Y	162 AsnIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle	222
0B	502 AAGTAAAGCTGCGACAGTACGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	562
0Y	182 LeuMetTyrSerTyrTyrTyrGlyLeuSer	242
0B	562 GTCATATAGCATATATCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	622
0Y	196 HisIleTyrIleGluIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle	256
0B	619 ----- AAAGCGTACATGACGACGACGCTTCAAGATGACGACGCTTCAAGAC	679
0Y	216 ThrIleThrHisThrLeuSerAlaValValLeuGluGluGluGluGluGluGluGluGlu	276
0B	661 ATGCTTTCGACAGCTCTTTCAGCATACCTCTTTCATATATATATATATATATATATAT	721
0Y	236 Ile	296
0B	721 CAGTTCCTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	781
0Y	256 ThrTyrArgLysLysIleValIleLysLysGlu	316
0B	781 AGCTATCTTAAAGAGCAAAAGCAAAAGCAAAAG	841

RESULT 12
 US-09-903-456-72 Application US/09904456
 Sequence 72, Patent No. US20020138874A1
 GENERAL INFORMATION:
 APPLICANT: Abbott Laboratories
 APPLICANT: Mukerji, Pradipt
 APPLICANT: Leonard, Amanda Eun Yeoung
 APPLICANT: Huang, Yung-Sheng
 APPLICANT: Peretta, Suzette L.
 TITLE OF INVENTION: FLOWNASH GENES AND USES THEREOF
 FILE REFERENCE: 6407 US, P4
 CURRENT APPLICATION NUMBER: 05/094903, 456
 CURRENT FILING DATE: 2001-07-11
 PRIOR APPLICATION NUMBER: US 09/624,670
 PRIOR FILING DATE: 2000-07-24
 PRIOR APPLICATION NUMBER: US 09/879,095
 PRIOR FILING DATE: 1999-08-23
 PRIOR APPLICATION NUMBER: US 09/145,828
 ERROR FILING DATE: 1998-09-02
 NUMBER OF SEQ ID NOS: 116
 SOFTWARE: FASTA for Windows Version 4.0
 SEQ ID NO 72
 LENGTH: 819
 TYPE: DNA
 ORGANISM: *Mycobacterium tuberculosis*
 US-09-903-456-72

Alignment Scores:	
Pred. No.:	2,36/36
Score:	403.5/50
Percent Similarity:	52.95%
Best Local Similarity:	43.70%
Query Match:	25/77
DH:	10


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QY 208 acglnLeuValGlnPheValLeuThrIleThrIsthrLeuSerAlaValValLysProCy 228
    |||||
    187 GCAGCTGCTTCACCTTGCTGACAACTATGATACCTGCGCGGCTGATCTGCGCGG 246
    |||||
QY 228 sglyPheProPheGlyCysLeuIlePheGlnSerSeryMetMetThrLeuValIleLe 248
    |||||
    247 CACATTCCTCTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 306
    |||||
QY 248 upheLeuAsnPhuTyrlleGlnPhuTyrlArgLysLysProValIlyslYslLeuGlnG 268
    |||||
    307 CTTCACAAACTCTTACATTCAGACCTACACACAGAAAGGCGCTCCCGAAGGAAAGACCA 366
    |||||
QY 268 u--LysGluValLysAsnGlyPheProLysAlaHisLeuIleValAlaAsnGlyMetTh 287
    |||||
    367 CCGTGAAGGACACACACATGCG-----TCCATGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 414
    |||||
QY 287 rAsp 288
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    415 CAAC 418
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Search completed: June 16, 2003, 01:12:52
Job time : 134.966 secs



GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

Ok protein - nucleic search, using frame_plus.p2n model

Run on: June 15, 2003, 21:36:46 ; Search time 163.06 Seconds

(without alignments)
4066.072 Million cell updates/sec

Title: US-09-624-670-63
Perfect score: 1567
Sequence: 1 MEOLKAFDEVNNAFLDNNMG. NCFPKAHIVAN:MTUKKQ 292

Scoring table:

BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Delop 6.0, Delext 7.0

Searched: 16154066 seqs, 8037743376 residues

Total number of hits satisfying chosen parameters: 33108132

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:

MODE=frame.p2n.model -DEV=slp
-O=/cgn2_1/USPTO.spool/US09624670/runat.1064003.075430.11642/app-query.fasta.1.110
DB=EST -OPMT=fastap -SUFFIX=est -MINMATCH=0.1 -LOOPEXT=0
UNITS=bits -START=1 -END=1 -MATPIX=biosum62 -TRANS=human40.cgi -LIST=45
LOCALALIGN=200 -THR_SCORE=est -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
OUTFM=ptio -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=200000000
USER=US09624670.ecgn.1.13724.ajrunat.11062003.075430.11642 -NCPU=6 -ICU=3
-NO_MMAR -LARGEQUERY -NRC_SCORES=0 -WALT -DSPLOCK=100 -LONLOCK
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -YGAPOP=6
-YGAPEXT=7 -YDELOP=10 -YDELEXT=0.5 -DELEXT=7

Database:

EST.*
1: em_vslha.*
2: em_gshum.*
3: em_estln.*
4: em_estmu.*
5: em_estrov.*
6: em_estrpl.*
7: em_estrv.*
8: em_hcl.*
9: qb_estl.*
10: qb_est2.*
11: qb_hic.*
12: qb_est3.*
13: qb_est4.*
14: qb_est5.*
15: em_estfun.*
16: em_estom.*
17: qb_gss.*
18: em_gss_hum.*
19: em_gss_inv.*
20: em_gss_pln.*
21: em_gss_vit.*
22: em_gss_fun.*
23: em_gss_mam.*
24: em_gss_mus.*
25: em_gss_other.*
26: em_gss_pro.*
27: em_gss_rod.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1562	99.7	1800	11 AK014803	AK014803 Mus musculus
2	1414	99.2	1150	13 BM461375	BM461375 AGNCNCOURT
3	1097	70.6	661	10 BB544040	BB544040 BB544040
4	1079	68.9	642	10 BB516155	BB516155 BB516155
5	1015	64.8	589	9 A1172603	A1172603 nt-p-cpp-
6	1008	64.3	654	13 B1598800	B1598800 B1598800
7	994	63.4	673	10 BB442845	BB442845 BB442845
8	962	61.4	645	10 BB414301	BB414301 BB414301
9	929	59.3	639	13 B1392770	B1392770 PFP1n PKO
10	922.5	58.9	941	9 AL559414	AL559414 AL559414
11	904	57.7	537	12 BE949059	BE949059 U1-M-BH3-
12	903.5	57.7	1088	12 BE778045	BE778045 B01463148
13	896	57.2	950	9 AL553407	AL553407 AL553407
14	887	56.6	861	9 AL514872	AL514872 AL514872
15	886	56.5	807	14 B2883763	B2883763 AGNCNCOURT
16	885	56.5	521	10 AW484100	AW484100 U1-M-BH3-
17	879	56.1	631	9 A1595258	A1595258 M14309.Y
18	879	56.1	893	14 BQ217076	BQ217076 AGNCNCOURT
19	877	56.0	504	12 BP41032	BP41032 U1-M-CGDP
20	871.5	55.6	900	13 B1593107	B1593107 B03344472
21	842.5	53.8	700	13 B1155440	B1155440 B03903816
22	840	53.8	619	9 A1760844	A1760844 AL740839
23	834	53.2	464	9 A1428150	A1428150 M14309.X
24	833	53.2	991	14 BQ945704	BQ945704 AGNCNCOURT
25	822	52.5	661	10 BB583165	BB583165 B04 B1062
26	811	51.5	745	9 A0079997	A0079997 A0079997
27	807	51.5	802	9 AL516234	AL516234 AL516234
28	802	51.2	499	9 A1225632	A1225632 U13113.Y
29	800.5	51.1	825	13 B1853179	B1853179 B03370527
30	792	50.5	607	13 B1559943	B1559943 B03246113
31	792	50.2	700	9 AL548756	AL548756 AL548756
32	785	50.1	461	12 B4700691	B4700691 U1-M-BH3-
33	781.5	49.4	847	14 BQ131770	BQ131770 AGNCNCOURT
34	781	49.4	747	13 B1597218	B1597218 B03250946
35	765	48.8	525	12 BQ813561	BQ813561 B0440407
36	764.5	48.8	844	13 B1785856	B1785856 B0407006
37	759	48.4	712	13 B0523961	B0523961 B0523961
38	754	48.1	445	9 A1815480	A1815480 B04604.Y
39	754	48.1	932	9 AL552819	AL552819 AL552819
40	744	47.5	862	13 B1635075	B1635075 B03081730
41	726.5	46.4	810	12 BQ251449	BQ251449 B03363905
42	714	45.6	748	12 BQ270622	BQ270622 B036009.Y
43	709.5	45.3	712	13 B0375432	B0375432 B03841085
44	706	45.1	961	14 B0346171	B0346171 AGNCNCOURT
45	706	45.0	927	12 B0173950	B0173950 B03344023

ALIGNMENTS

RESULT 1
AK014803
LOCUS
DEFINITION
AK014803 3800 bp mRNA linear HTG 19-FAN-2002
Mus musculus adult male testis cDNA, RIKEN full-length enriched
library, clone:4921503C17, elongation of very long chain fatty acids
(FEN1/R102, SUR4/E103, yeast) like 2, full insert sequence.
ACCESSION
AK014803
VEPSTON
AK014803 1 51-12852861
HTG: CAP Trapper.
KEYWORDS
Mus musculus (strain:G57BL/6J) adult male testis cDNA to mRNA,
clone:4921503C17.
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE	AUTHORS	TITLE
JOURNAL MEDLINE PUBMED REFERENCE	Carninci, P. and Hayashizaki, Y.	High efficiency full length cDNA cloning Methods. Enzymol. 403, 19-44 (1999)
JOURNAL MEDLINE PUBMED REFERENCE	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.	Normalization and subtraction of cap-trapper selected cDNAs to prepare full length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
JOURNAL MEDLINE PUBMED REFERENCE	Shibata, K., Itoh, M., Aizawa, K., Naraoka, S., Sasaki, N., Carninci, P., Kono, H., Akiyama, J., Nishi, K., Kitsuana, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishio, T., Harada, A., Yamamoto, R., Matsumoto, H., Sadaquchi, S., Ikegami, T., Kashiwagi, K., Fujisawa, S., Inoue, K., Toiyama, Y., Iawa, M., Ohara, E., Watanabe, Y., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanabe, T., Matsuda, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kita, A. and Hayashizaki, Y.	RIKEN integrated sequence analysis (RISA) system 384-format sequencing pipeline with 484 multiplexillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
JOURNAL MEDLINE PUBMED REFERENCE	Kawai, J., Shibata, K., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Aizawa, T., Hara, A., Fukunishi, Y., Kono, H., Adachi, J., Fukuda, S., Aizawa, K., Iawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamada, I., Saito, T., Okazaki, Y., Goshobori, T., Honjo, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, P., Fleischmann, W., Gastroland, T., Gissi, C., Kling, B., Kochiwa, H., Kuchi, P., Lewis, S., Matsuo, Y., Nika, D., I. Pesole, G., Quakebush, J., Schriml, L. M., Staehli, F., Suzuki, K., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okino, T., Furuno, M., Aono, H., Baldarelli, R., Barish, G., Blake, J., Bottelli, D., Bojunga, N., Carninci, P., de Bonaldo, M. F., Brownstein, M. J., Bulc, C., Fletcher, C., Fujita, M., Gariboldi, M., Gastinich, S., Hill, D., Hofmann, M., Hume, D. A., Kamiya, M., Lee, N. P., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, L., Monbaldi, P., Nordone, P., Rijn, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schombach, J., Sessa, T., Shibata, Y., Storch, K. F., Suzuki, H., Toyooka, K., Wang, K. H., Wolff, C., Whitaker, C., Wilming, L., Wyshak, B. O. S. A., Yoshida, K., Hasegawa, Y., Kawai, H., Kohsaki, S. and Hayashizaki, Y.	Functional annotation of a full-length mouse cDNA collection Nature 409 (6821), 645-649 (2001)
JOURNAL MEDLINE PUBMED REFERENCE	Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Arakawa, T., Baldarelli, R., Itoh, H., Brownstein, M., Bull, C., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanaoka, T., Hara, A., Hayatsu, N., Hill, D., Hiramoto, K., Hiraoka, T., Hori, F., Hume, D., Imotani, K., Ishii, Y., Itoh, M., Iwada, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kono, H., Kondo, M., Koya, S., Kurihara, C., Matsuyama, J., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, K., Ono, M., Okazaki, Y., Okido, T., Owa, C., Quakebush, J., Saito, H., Saito, R., Sakai, K., Sakai, K., Sano, H., Sasaki, D., Schriml, L., Shibata, K., Shibata, Y., Shinagawa, A., Shikata, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Toiyama, Y., Toyai, I., Yamamura, T., Yamada, I., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.	Direct submission Submitted (10-JUL 2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suoh-cho, Tsukuba, Ibaraki, 305, Yokohama, Kanagawa 240 0045, Japan (E mail: genome-resgsc@riken.go.jp, URL: http://www.t.riken.go.jp/ Tel: 81 47 502 4222

[illegible]

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 QY 102 LeuAspSerAlaCysIleGluGlyAspValArgValAlaLysValLeuTrpTrpTyrPhe 121
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 QY 142 IleThrPheLeuHisValIleThrHisHisAlaSerMetPheAsnIleTrpTrpCysValLeu 161
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 QY 162 AsnTrpIleProCysGlyIleSerPhePheGlyProThrLeuAsnSerPheIleHisIle 181
 D 609 AACTGCATACCTCTGCTGCTCAAACTCTTGTGACCCACCTCAACACCTTTATCCACAT 668
 QY 182 LeuMetLysSerTyrTyrGlyLeuSerValPheProSerMetHisLysTyrLeuTrpTrp 201
 D 669 CTGATGACTACCTACTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 728
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 SOURCE house mouse.
 ORGANISM Mus musculus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 1150)
 AUTHORS NIH-MGC. <http://mgc.ncl.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 CONTACT: Robert Strausberg, Ph.D.
 Email: cgaps-f@mail.nih.gov
 Tissue Procurement: Aaron Haeub
 COMMENT cDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution, MGC clone distribution information can be
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<http://image.llnl.gov>
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 this is a NCLCGAP Library."

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 ORIGIN

Alignment Scores:
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 Score: 1414.00 Matches: 274
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US-09-624-670-63 (1-292) x BM461375 (1-1150)

QY 12 AsnAlaPheLeuAspAsnMetPheGlyProAlaGlyAspSerArgValArgGlyTrpPheLeu 31
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 QY 32 LeuAspSerTyrLeuProThrPheIleLeuThrIleThrTyrLeuLeuSerIleTrpLeu 51
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	BB654040		

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version      BB654040.1  (31:16487868)
extending    0

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SOURCE:
ORGANISM

REFERENCE AUTHORS

TITLE:
JOURNAL:
COMMENT:

Bukacinski A., Morozova Khorontsa; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus; 1 (bases 1 to 661)

Arikawa, T., Carollini, P., Fukuda, S., Furumoto, M., Hanagaki, T., Hara, A., Hiramoto, K., Horii, F., Ishii, Y., Ito, M., Kaaiji, J., Kitano, H., Kouda, M., Koyama, S., Matsuyama, T., Miyazaki, A., Nemura, K., Ono, H., Okazaki, Y., Ohtsu, I., Saito, R., Sakai, C., Sakai, K., Sato, H., Sasakawa, D., Shibata, K., Shinawana, A., Shiraki, T., Sobue, Y., Suzuki, H., Tagami, M., Takawa, A., Takahashi, F., Takada, Y., Tanaka, T., Toyota, T., Muramatsu, M. and Hayashizaki, Y.

RIKEN Mouse ESTs (Arakawa, T. et al 2001)
Unpublished (2001)

Contact: Yoshihide Hayashizaki
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1-7-22, Suwhiro-cho, Tsurumi-Ku, Yokohama, Kanagawa 230 0045, Japan
Tel.: 81 45 508 9222;
Fax: 81 45 508 9211
E-mail: genome_research@iken.go.jp/
URL: <http://genome.riken.go.jp/>
carrollin, P., Shibata, Y., Hayatsu, K., Sugahara, Y., Shibata, K., Itoh
M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1640 (2000)

Waei, K., Fujiwara, S., Inoue, K., Tezawa, Y., Izawa, M., Ohara, E.,
Matsumi, M., Oyada, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunaga,
S., Kawaji, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kita, A. and
Hayashizaki, Y.

RIKEN integrated sequence analysis (RISA) system 384 format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)

Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carroll, P., Sugahara,
Y. and Hayashizaki, Y.

Computer based methods for the mouse full length cDNA
encyclopedia: real time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

Kondo, S., Shintawara, A., Saito, T., Kiyosawa, H., Yananaka, I., Alizawa,
K., Fukuda, S., Hara, A., Itoh, M., Kawaji, J., Shibata, K. and
Hayashizaki, Y.

Computational Analysis of Full-length Mouse cDNAs Compared with
Human Genome Sequences. Mamm. Genome 12, 674-677 (2001)

PLEASE VISIT OUR WEB SITE (<http://www.gscn.com.au>) FOR FURTHER DETAILS.
E MOUSE ISSUES:
Location/Qualifiers
1. 661

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Project of Genome Exploration Research group in Riken
Genomic Sciences Center and Genome Science Laboratory in

```

R. KIKEN, Division of Experimental Animal Research, In Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5].

GAGGACGAGGAGCGCCGCCATCTGCAGTTTTCCTTTTTCVN 3'. cDNA was prepared by using reverse-transcriptase activated reverse transcriptase and subsequently enriched for full length by

capped trapper. Second strand cDNA was prepared with the primer adapter of sequence 15' GGAAGAAGATCTGGATTATTAATTATTCCTCCCTCCCTC 3'. cDNA was cleaved with BamHI and XhoI. Vector: a modified pBlueScript KS(+) after bulk excision from Lambda EucT1. Tissue was provided by William A. Held, Kosciuszko Park

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ORIGIN
Cancer Institute, Department of Molecular and Cellular
Biology, Elm and Carlton Streets, Buffalo, NY 14263, WHO'S
assistance we gratefully acknowledge."

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US-09-524-670-63 (1.292) x HB64040 (1.661)

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Gy 61 AATAGGCTGATAGGATTTTCTGGTATCTGATGATGATGATGATGATGATGATGATGAT 80

Db 227 GCTGTCT 286

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 QY 101 AsnIuAspSerAidcIgcIucIgcIAspValArGValAlaIAspValIcuIprIprItyr 120
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RESULT 4
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 SOURCE house mouse.
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 642)
 Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanzaki, T., Hara, A.,
 Hiramoto, K., Horii, F., Ishii, Y., Ito, M., Kawai, J., Kono, H., Kudo,
 M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ono, M., Otake,
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 D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H.,
 Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toyota, T.,
 Muramatsu, M. and Hayashizaki, Y.
 RIKEN Mouse ESTs (Arakawa, T., et al. 2001)
 Unpublished (2001)
 Contact: Yoshinide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic
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 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suenryo-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@gsr.riken.go.jp,
 URL: http://genome.gsc.riken.go.jp/
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh,
 M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new
 genes. Genome Res. 10 (10), 1617-1630 (2000)
 Wagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,
 Watanabe, M., Yoneda, Y., Ishikawa, T., Oizawa, K., Tanaka, T., Matsuda,
 S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and
 Hayashizaki, Y.
 RIKEN integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multiplexed sequencer. Genome Res. 10
 (11), 1757-1771 (2000)
 Kono, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara,
 Y. and Hayashizaki, Y.
 Computer-based methods for the mouse full-length cDNA
 encyclopedia: real-time sequence clustering for construction of a
 nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
 Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamaoka, I., Aizawa,
 K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
 Hayashizaki, Y.
 Computational Analysis of Full-length Mouse cDNAs Compared with
 Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
 Please visit our web site (http://genome.gsc.riken.go.jp) for
 further details.
 e mouse tissues.

FEATURES

Source

Location/Qualifiers

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 Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in
 RIKEN. Division of Experimental Animal Research in Riken
 contributed to prepare mouse tissues. 1st strand cDNA was
 primed with a primer (5'
 GAGAGAGAGAGAGATCCAGAGAGCTTTTCTTTTCTTTTCTTN 3'). cDNA was
 prepared by using Tethanolase thermo-activated reverse
 transcriptase and subsequently enriched for full-length by
 cap-trapper. Second strand cDNA was prepared with the
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 GAGAGAGAGAGAGAGAGATCCAGAGAGCTTTTCTTTTCTTTTCTTN 3'). cDNA was cloned into the XhoI and BamHI sites."
 BASE COUNT 139 a 172 c 151 g 179 t
 ORIGIN
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 Score: 1079.00 Matches: 203
 Percent Similarity: 98.54% Conservative: 0
 Best Local Similarity: 98.54% Mismatches: 1
 Query Match: 68.86% Indels: 2
 DB: 10 Caps: 0

US-09-624-670-63 (1-292) x BB616155 (1-642)

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 D1b 88 CCAGAGATTCCTCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 147
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 D1b 428 AATTCATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 387
 Q1 121 PheSerTyrLeuValGluPheLeuAspPheIlePhePheValLeuArgLysTyrAsn 140
 D1b 388 TTCTTCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 447
 Q1 141 GlnIleThrPheLeuHisValTyrHisHisAlaSerMetPheAsnIleTrpGlyVal 160
 D1b 448 CAGATTCATCTTCATGCTATGACACACCGGTCGCAATGTCACATGTCGCTGCTGCTGCTGCT 507
 Q1 161 LeuAsnTrpIleProGlyGlnSerPhePheGlyProThrLeuAsnSerPheIleHis 180
 D1b 508 TTGAATTCGATACCTGTGTGGCAAGCTCTTTGGACCCCTAGACAGCTTTATCCAC 567

Tissue Procurement: Miklos Palokovits, M.D., Ph.D.
 cDNA Library Preparation: Michael J. Brownstein (NHRI), Shiroki
 Toshiyuki and Piero Carninci (RIKEN)
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNI)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/ILNI at:
<http://image.llnl.gov>
 plate: LHAM1777 row: 6 column: 19
 High quality sequence stop: 669

FEATURES

SOURCE

Location/Qualifiers

1..664

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAG:5287890"

/clone_lib="NIH_MGC_96"

/tissue_type="hypothalamus"

/lab_host="DH10B"

/note="Organ: Brain; Vector: pBluescriptR (modified
 pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (qtcgaq
); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTVN-3',
 size-selected for average insert size 2.3 kb and
 normalized to 10⁷ 5. This is a primary library enriched
 for full-length clones and constructed using the
 Cap-trapper method (Carninci, in preparation). Library
 constructed by M. Brownstein (NHRI/NHRI, National
 Institutes of Health). Note: this is a NIH_MGC Library."

BASE COUNT

160 a 163 c 156 g 205 t

CRIGIN

Alignment Scores:

Score: 1.22e-105 Length: 684
 Percent Similarity: 1008.30 Matches: 182
 Percent Similarity: 95.988 Conservative: 9
 Percent Similarity: 91.468 Mismatches: 8
 Query Match: 64.338 Indels: 0
 DB: 13 Gaps: 0

US-09-624-670-63 (1-292) x B1598800 (1-684)

1 MetGluLeuLeuysAlahhcasPasncluvAlaAlaPhelcuAspasmethocy 20
 76 ATGGACATCTAAAGCCCTTGTATGATGAATCAATGCTTTTGGACAAATAGTGGAA 135
 21 ProArgAspSerArgValArgGlyTrpPheLeuAspSerTyrLeuProthrhelle 40
 136 CCGGAGATTCGAGACAGCGGCTGCTTCAATGCTGACCTTACCTCTCTCTCTTT 195
 41 LeuThrIleThyTyrLeuSerIleTlePleuGlyAsnLysTyrMetLysAsnPro 60
 196 CTACAGTCATATATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 255
 61 AlaLeuSerLeuArgGlyIleLeuThrlcuTyrAsnLysAlaIleThrlcuLeuSer 80
 256 GCTCTTCTCTTAAAGGATATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 315
 81 TyrMetLeuValGluLeuIleLeuSerTyrPglucGlyTyrAsnLeuIleGlyGln 100
 316 TACCTGCTGCGACAGCTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 375
 101 AsnLeuAspSerAlaGlyIleGlyAspValArgValAlaIleValLeuTrpTrpTyr 120
 376 GATCTTACACCGCGAGCGAGCTGACATTCGCGGATGCGCAACGCTGCTGCTG 435
 121 PheSerLysLeuValGluPheLeuAspThrIlePhePheValLeuArgLysLysThrAsn 140
 436 TTCTCCAAATCAGTAGAGTTCTGAGACACAAATTTTCTCTCTTGGGAAAAAGAGAT 495
 141 GluIleThrlPheLeuThsValTyrThsAlaSerMetPheAsnIleTrpTrpCysVal 160
 496 CAGATTACTTCT 555
 161 LeuAsnTrpIleProCysGlyLysSerPhePheGlyProThrlcuAsnSerPheIleHis 180

181 IleLeuMetTyrSerTyrTyrClyLeuSerValPheProSerMetHisLysTyrLeu 199
 616 ATTATTATCT 712

RESULT 7

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

SOURCE

LOCATION/Qualifiers

1..673

/organism="Mus musculus"

/db_xref="taxon:10090"

/clone="A93004JF19"

/clone_lib="RIKEN full-length enriched, adult retina"

/tissue_type="retina"

/dev_stage="adult"

/lab_host="DH10B"

/note="Site_1: SalI; Site_2: BamHI; cDNA library was

181

616

ATTATTATCT

712

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ATTATTATCT

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ATTATTATCT

712

COMMENT

Contact: Chin, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N 7190, MSC 9643, Bethesda, MD
20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9690
Email: MEStf@mail.nih.gov
Oligo dT track not found. Not a site shown in beginning of sequence.
Is likely internal to the message cDNA Library Preparation: M.R.
Soares Lab Clone distribution: Researchers may obtain BMAP cDNA
clones from RESEARCH GENETICS. It should be noted that Bento Soares
is generating a small number of additional specialized
non-redundant arrays of BMAP cDNAs whose availability will be
considered under appropriate and limited collaborative arrangements.
Seq. primer: M13 forward
SOLiA-No.


```

D1) 719 AAGTACATCATCGAGGCGAAGCTGCTTCAGTTTGGTGGCAATATCAACAGACACACCTGC 778
Q* 223 AAlaValAlaLysProCysTllyPheProPheGlyCysLeuLeuPheGlnInsertSerTrpC 242
D1) 779 GGGGTATCTGGCCGTCGACATCTCCCTTGGTGG-CTGTATTTCAGATTGCAATACAG 837
Q* 243 MetThrLeuVal:leuPheLeuAsnMetPheTllyLeuGlnThrTyrArgLys-LysProVa 262
D3 838 ATTCCCTGATTGCTGCTCTTCCACAAAGCTTACATTACAGCTACACCAAGAAAGGGGCT 897
Q* 262 LlysLysGluLeuGlnGlnLysGluValAlaLysAsnGly 274
D3 898 CCCAAGGAAAGACACACTGAACGACCCAGAAATGGT 934

RESULT 14
LOCUS AL514872 861 bp mRNA linear EST J3-PBR 200
DEFINITION prime_mRNA sequence.
ACCESSION AL514872
VERSION AL514872.1 GI:12778365
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE L1, W. B., Gruber, C., Jessee, J. and Polayes, D.
FULL-LENGTH cDNA LIBRARIES AND NORMALIZATION
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web www.genoscope.cns.fr.

FEATURES
SOURCE
1..661
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="LCDBB0142F12"
/clone_11b="L1-NFL006.PL2"
/tissue_type="placenta"
/vector="Vector: pCMVSPORT 6, Site: J. NotI, 1st strand cDNA
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies, Contract: Feng Liang Life Technologies
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax: (1) 301 610 8371
Email: lliang@litech.com URL:
http://www.length.invitrogen.com"

BASE COUNT 193 a 232 c 180 g 256 t
ORIGIN
Alignment Scores:
Pred. No.: 1,49e-91 Length: 861
Score: 887.00 Matches: 155
Percent Similarity: 76.19% Conserved: 37
Best local Similarity: 61.51% Mismatches: 60
Query Match: 56.60% Indels: 1
DB: 9 Gaps: 0

US-09-624-670-63 (1-292) x AL514872 (1-861)
QY 3 GlnLeuLysAlaPheAspAsnGluValAsnAlaPheLeuAspAsnMetPheGlyProArg 22
D1 105 CAAATGGAACATTTGATTCATCATCAGCTTACTAGCTATTTCACAGGACATTCAGCCCTCGA 164
QY 23 AspSerThrValAlaGlyTyrPheLeuLeuAspSerTyrLeuProThrPheLeuThr 42
D1 165 GATACATGAGGTAAAGAGATGCTTCTCTTCGACAAATTATATACCACTTATCTGCTCT 224

```

[illegible]

GenCore version 5.1.6
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OV protein - nucleic search, using frame_plus.p2n model

Run on: June 15, 2003, 21:11:36 ; Search time 2216.45 Seconds
(without alignments)
3925.989 Million cell updates/sec

Title: US-09-624-670-64
Perfect score: 1651
Sequence: 1 MHPDASLSTFKAFKLPD.... HTNSPSPLENSVPRKPKU 299

Scoring table:
BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:
-MODE=frame+2n.model -3V-XLP
-2/cg2.1/USPTO/US03624670/runat.11062003.075430.11630/app.query.fasta.1.910
-DB=GenEmbl -OPMT=fastap -SUPERX-rge -MINMATCH=0.1 -LOOPTC=10 -LOOPTXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR=SCORE-pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pro -NOR=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2100000000
-USPR=US03624670.#CGN.1.1.3854.#runat.11062003.075430.11630 -NCPU=6 -ICPU=3
-NO_MMAP -LARCORDERY -NFG -SCORES=0 -WAIT -DSPHLOCK=100 -10NGILOG
-DEV_TIMEOUT=120 -MAPN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELCP=6 -DELEXT=7

Database :
1: GenEmbl:*
2: gb_da:*
3: gb_hg:*
4: gb_in:*
5: gb_om:*
6: gb_ov:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_rc:*
11: gb_sts:*
12: gb_sy:*
13: gb_ur:*
14: gb_vl:*
15: em_da:*
16: em_hu:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_ov:*
22: em_ph:*
23: em_pl:*
24: em_pr:*
25: em_rc:*
26: em_sts:*
27: em_sy:*
28: em_un:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description
1	1651	100.0	900	6	AX464735 Sequence
2	1647	99.8	2702	10	BC032911 Mus muscu
3	1577	95.5	900	10	AB071985 Rattus no
4	1559	94.4	900	9	AF231981 Homo sapi
5	1558	94.4	2257	9	HS0601903 Homo sapi
6	1558	94.4	3011	9	AF338241 Homo sapi
7	1558	94.4	914	6	AX464732 Sequence
8	1557	94.3	2592	6	105465 Sequence 1
9	1557	94.3	2592	6	AP465629 Sequence 1
10	1156	70.0	1397	5	AX127718 Sequence
11	1148	69.5	925	6	AX464734 Sequence
12	956.5	57.9	879	6	AF170608 Mus muscu
13	956.5	57.9	3708	10	AF170608 Mus muscu
14	956.5	57.9	3795	6	AX052773 Sequence
15	956.5	57.9	2340	9	AK000341 Homo sapi
16	669	40.5	2868	10	AF277093 Mus muscu
17	653.5	39.6	945	6	AX467496 Sequence
18	653.5	39.6	2219	9	AK055277 Homo sapi
19	653.5	39.6	2000	9	AF277094 Homo sapi
20	653.5	39.6	2992	9	AY047298 Homo sapi
21	653.5	39.6	3983	6	AX430266 Sequence
22	653.5	39.6	3415	6	AX402493 Sequence
23	650.5	39.4	3072	9	AR063100 Mus muscu
24	586	35.5	2485	14	AF194100 Homo sapi
25	541.5	32.8	1986	3	AY119173 Homo sapi
26	516	31.3	2065	3	BC017270 Homo sapi
27	505	30.6	86794	5	AC036019 Homo sapi
28	498	30.2	2580	3	AY060267 Homo sapi
29	484	29.3	846	6	AX467489 Sequence
30	476	28.9	1486	9	BC000618 Homo sapi
31	474.5	28.7	1457	9	AK001653 Homo sapi
32	474	28.7	1684	3	AY060447 Homo sapi
33	472	28.6	1840	10	BC006602 Homo sapi
34	471.5	28.6	949	6	AX052771 Sequence
35	471.5	28.6	1471	9	AF336793 Homo sapi
36	467	28.3	1471	9	AF151846 Homo sapi
37	462.5	28.0	1137	10	BC006735 Mus muscu
38	462.5	28.0	1468	10	AF170607 Mus muscu
39	462.5	28.0	1488	9	AX052779 Sequence
40	451	27.3	2508	9	AK027416 Homo sapi
41	448	27.1	2091	17	AF111849 Homo sapi
42	431.5	26.1	1595	3	AY061182 Homo sapi
43	426	25.8	2018	3	AF173627 Homo sapi
44	425.5	25.8	50374	2	AC015170 Homo sapi
45	425.5	25.8	164193	4	AY064944 Homo sapi

RESULT 1

ALIGNMENTS


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/db_xref="GI:18605605"
/translation="MEHFDASLSTYFKALGPDRTRVKGWFLDNTPTFVGSVITLL
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GESDMKIIIVLWYYSKLIEMDFEFLIRKNHOTTIVHVAHMLIMFVNMW
VPGHSYFPGATLNSF IHLVIMSYGLSVPSPMRBYLWKKYIIOGOLVQVLI I OTT
CGVIMPSFPLGLMFLFOIGYMSLIALTPTNFIOTYNNKKSRRRHHKOHONGSVA
VNCHTNSPFLNSVSKPRKORKD"
BASE COUNT      710 a      607 c      577 g      808 t
ORIGIN
Alignment Scores:
  Pred. No.:      8,32e-152      Length:      2702
  Score:          1647.00         Matches:      298
  Percent Similarity: 100.00%     Conserved:    1
  Best Local Similarity: 99.67%   Mismatches:  0
  Query Match:    99.76%         Indels:      0
  DB:             10             Gaps:         0
US-09-624-670-64 (1-299) x BC022911 (1-2702)
Q7      1 MetGluHisPheAspAlaSerLeuSerThrTyrrPheValAlaPheLeuGlyProAlaAsp 20
        |||||||
D3      80 ATGGACAAATTTCCATGGCTGCTACTGACTATTTCAGGCGCTTCTCGCCCGGAGAT 139
        |||||||
Q7      21 ThrArgValIysGlyTrpPheLeuLeuAspAsnTyrIleProThrPheValCysSerVal 40
        |||||||
D3      140 ACAAGAGTCAAAGATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 193
        |||||||
Q7      41 IleTyrLeuLeuLeuValIleTyrPheGlyProLysTyrMetLysAsnArgGlnProPheSer 60
        |||||||
D3      200 ATTACTACTACATTCATTTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 259
        |||||||
Q7      61 CysArgGlyIleLeuGlnLeuTyrAsnLeuGlyLeuThrLeuLeuSerLeuTyrMetPhe 80
        |||||||
D3      260 TGCCGAGGACATCTGCGACTGTTGTAACCTTGCACTACCTGCTGCTGCTGCTGCTGCTGCT 319
        |||||||
Q7      81 TyrGluLeuValIleThrGlyValIleTyrGlyLysTyrAsnPhePheCysGlnIleThrArg 100
        |||||||
D3      320 TATGAGTGTGACAGGAGTGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 379
        |||||||
Q7      101 SerAlaGlyIleGluSerAspMetLysIleIleArgValLeuTyrPheTyrPheSerLys 120
        |||||||
D3      380 ACCGGGGAGAAATCGCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 439
        |||||||
Q7      121 LeuIleGluPheMetAspThrPhePhePheIleLeuArgLysAsnAsnHisGlnIleThr 140
        |||||||
D3      440 CTCATCGAATTCATGACACCTTTCTCTCATCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 499
        |||||||
Q7      141 ValLeuHisValTyrHisHisAlaThrMetLeuAsnIleTyrTrpPheValMetAsnTrp 160
        |||||||
D3      500 GTGCTCCATGCTGACACGACGCTACCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 559
        |||||||
Q7      161 ValProGlyGlyHisSerTyrPheGlyAlaThrLeuAsnSerPheIleHisValLeuMet 180
        |||||||
D3      560 GTTCCCTGGGCGCATTCATATTGTTGCTGCGACCTCAACAGCTTCATCCATGCTGCTCATG 619
        |||||||
Q7      181 TyrSerTyrTyrGlyLeuSerSerIleProSerMetLysProTyrLeuTyrPheLys 200
        |||||||
D3      620 TACTGCTACTATGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 679
        |||||||
Q7      201 TyrIleThrGlyGlyLeuValGlnPheValLeuThrIleIleGlnThrPheCysGly 220
        |||||||
D3      680 TACATACACTCAAGGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 739
        |||||||
Q7      221 ValPheTrpProCysSerThrPheProLeuGlyTyrPheLeuPheGlnIleCysTyrMetIle 240
        |||||||
D3      740 GTCTTCTGGCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 799
        |||||||
Q7      241 SerLeuIleAlaLeuPheThrAsnPheTyrIleGlnThrTyrAsnLysLysGlyAlaSer 260
        |||||||
D3      800 TCCCTGATTCGCTCTTTCACAAACTTCATACATTCAGACTTACACAGAGAAAGGGGCGCTCT 859
        |||||||

```

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QY      261 ArgArgLysAspHisLeuLysGlyHisGlnAsnGlySerValAlaIleValAsnGlyHis 280
        |||||||
DB      860 CGGAGAGAAAGAACCTCGAAGAGGCGCACGAGAGAGGAGTGTGTTGGCGCGCTGACAGGAGATC 919
        |||||||
QY      281 ThrAsnSerPheProSerLeuGlnAsnSerValIleProArgLysGlnArgLysAsp 299
        |||||||
DB      920 ACCAACACCTTCCTCCCTCGAAGAACGCTGTAAGCCAGGACAGCAGCAAGAGAT 976
        |||||||
RESULT 3
AB071985
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
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AUTHORS
TITLE
JOURNAL
FEATURES
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1..900
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1..900
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IWLGRKYNRQPSKGILOLYNLGTLILSTLMEFLVGVGWEKYNFECGRTSA
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VPGHSYFPGATLNSF IHLVIMSYGLSVPSPMRBYLWKKYIIOGOLVQVLI I OTT
CGVIMPSFPLGLMFLFOIGYMSLIALTPTNFIOTYNNKKSRRRHHKOHONGSMTA
VNCHTNSPFLNSVSKPRKORKD"
BASE COUNT      210 a      243 c      207 g      240 t
ORIGIN
Alignment Scores:
  Pred. No.:      1.84e-145      Length:      900
  Score:          1577.00         Matches:      282
  Percent Similarity: 97.32%     Conserved:    9
  Best Local Similarity: 94.31%   Mismatches:  8
  Query Match:    95.52%         Indels:      0
  DB:             10             Gaps:         0
US-09-624-670-64 (1-299) x AB071985 (1-900)
QY      1 MetGluHisPheAspAlaSerLeuSerThrTyrrPheValAlaPheLeuGlyProAlaAsp 20
        |||||||
DB      1 ATGGACAAATTTCCATGGCTGCTACTGACTATTTCAGGCGCATTTACGGGCGCGGAGAT 60
        |||||||

```



```

/organism="Mus musculus"
/strain="BALB/c"
/db_xref="taxon:10090"
/sex="male"
/tissue_type="liver"
/dev_stage="9-11 weeks"
1..3708
/gene="Ssc2"
37..915
/gene="Ssc2"
/function="putatively involved in fatty acid elongation"
/feature="membrane protein"
/codon_start=1
/product="Ssc2"
/protein_id="AAF2573.1"
/db_xref="GI:8101521"
/translation="MRQLKALDENYNAHLLNNHPCIKSVKVM-ILDSYLPFLILLI
YLSLWGNKIKNRFALSLRGLITLILNLAITLSAIVLVELILSSMGGNLOQNL
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LNMIKCSQSEFGETLNSFLHILMSYSGVSPSMKYLMMKRLTLOLQVFLIT
HLSAVKPCGPPHCOLIPQSSYMMILVILINFLYLIYKPKPKPKPKPKPKPK
KAHLIVANGMTTKKAO"
BASE COUNT      984 a      867 c      779 g      1078 t
ORIGIN
Alignment Scores:
Pred. No.:      5 556-84      Length:      3708
Score:          956.50      Matches:      168
Percent Similarity: 71.58%      Conservative: 36
Best Local Similarity: 58.95%      Mismatches: 78
Query Match:    57.93%      Indels:      3
Db:             10      Gaps:      1
US-09-624-670-64 (1-299) x AF170908 (1-3708)
QY      1 MetGluHspheaspIasSerLeuSerThrTyPheYalaPheLeuGlyProArgSP 20
DB      46 CTGAAGGCGTTGGATATGACATGCAATGCTTCTGGACACATGTTTGAACGAGAT 105
QY      21 ThrArgValIysGlyTrpPheLeuLeuAspAsnTyrlleProthPheValCysSerVal 40
DB      106 TTCGAGATTGCGGAGTGGTCTGCGGACTCTTACCTCCGCACTTATCTTACCATC 165
QY      41 lletyrleuLeuValItrPheuglyProlystYrMetLysAsnArgGlnProPheSer 60
DB      166 ACGTACCTGCTCGATATGCGGCTGGAACACATCATCAAGACAGCGCTGCTGCT 225
QY      61 CysArgGlyIleLeuGlnLeuTyfAsnLeuGlyLeuThLeuLeuSerLeuTyfMetPhe 80
DB      226 CTAGAGAGCATGCTACATGTATAACTTGAATTAATTAATTTTTPAATATATG 285
QY      81 TyrcIleuValItrGlyValItrPgluclyLysfyrAsnphcheGcysGlnGlythrArg 100
DB      286 GTGAGATTAATGCTTTCGATGATGAGAGAGAGATTAATTAATTAATTAATTAAT 345
QY      101 SerAlaGlyLusSaraspMelLysIleIleArgValIleuTrpTrpTyfPheSerLys 120
DB      346 AGTCGACGAGACAGATGATGTCGCGTACGACGATCTTGTGGTACATCTTCACAA 405
QY      121 LeuIleGluPheMetAspTrpPhePhePheIleLeuArgLysAsnAsnIleGlnIleTr 140
DB      406 CTATGAGAGTTCGAGACATATTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 465
QY      141 ValIleuHsValItrHsIleSalIleTrMetLeuAsnIleTrpTrpPheValMetAsnTrp 160
DB      466 TTCCTGATGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 525
QY      161 ValProGlyIleHsSerTyfPheGlyAlaThrLeuLeuAsnSerPheIleHsValIleMet 180
DB      526 ATACCTTGCTGATCAACCTCTTGGACCCACCCGTAACAGCTTTTACACATTCGATG 585
QY      181 TyrcIleuValItrGlyLeuSerSerIleProSerMetArgProtyfLeuTrpTrpLys 200

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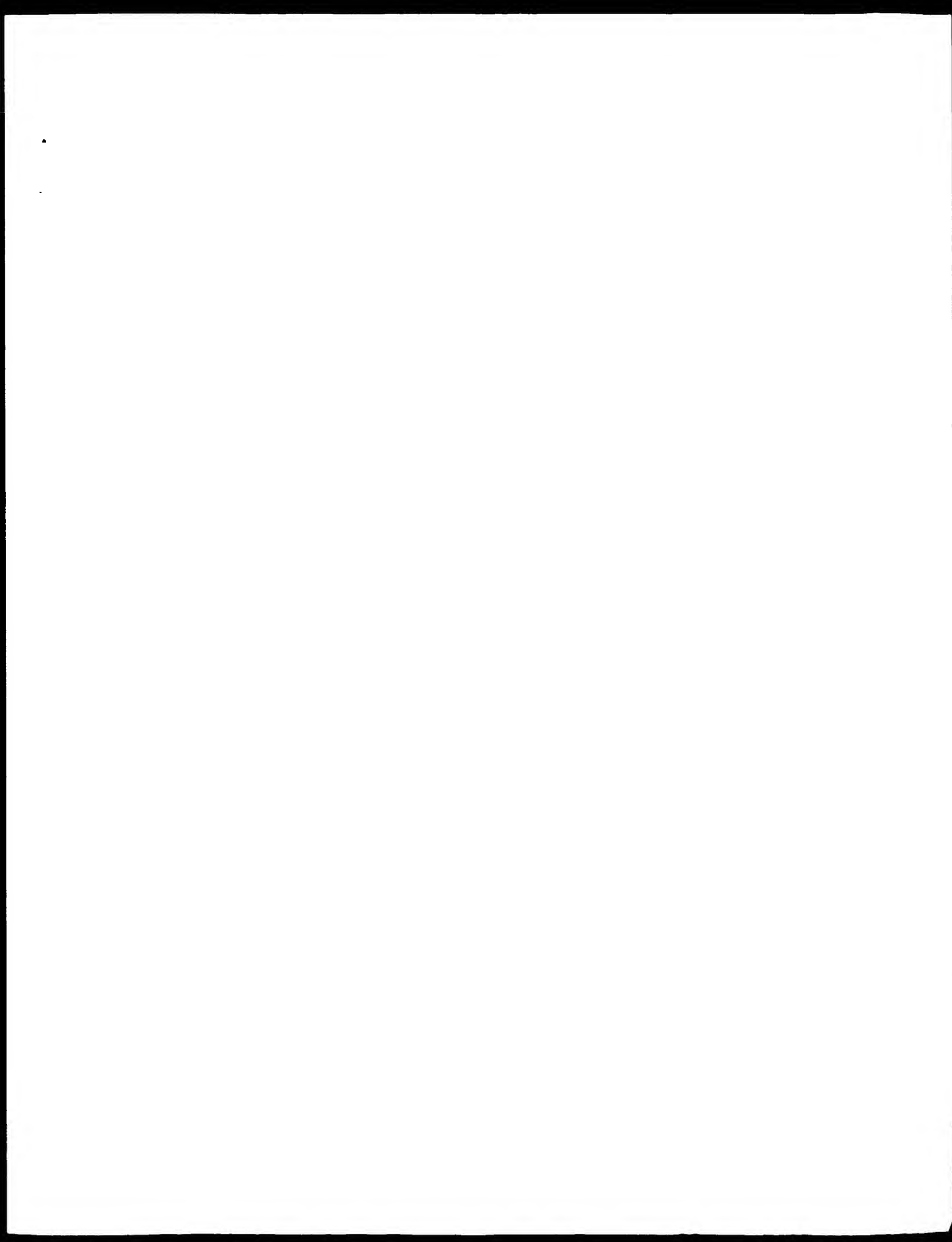
DB      586 TACTGCTATATGAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 645
QY      201 TyrcIleuHsValItrGlyLeuValGlnPheValIleuTrpTrpTyfPheSerLys 220
DB      646 TACCTGACAGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 705
QY      221 ValPheTrpProGlySerPhePhePheLeuGlyTrpPhePhePheIleGlyTyfMetIle 240
DB      706 GTGCTGACAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 765
QY      241 SerLeuIleAlaIleGlnPheThrAsnPheTyfIleGlnTrpTrpAsnLysGlyAlaSer 260
DB      766 ACGTGTATATGCTGTATATGCTGTATATGCTGTATATGCTGTATATGCTGTATATG 825
QY      261 Arg      ArgLysAspHsIleuGlyGlyIleGlnIleGlnIleGlnIleGlnIle 277
DB      826 AAAGACGCTGACAGACAGACAGACAGACAGACAGACAGACAGACAGACAGACAG 885
QY      278 AsnGlyHsIleThrAsn 282
DB      886 AATGCTATGACGCTGAG 900
RESULT 14
AX052773      3795 bp      DNA      linear      PAF 12-1AN-2001
LOCUS
DEFINITION
Sequence 5 from patent WO00/0945.
AX052773
VERSION
AX052773.1 GI:12226935
SOURCE
ORGANISM
Mus sp.
Eukaryota; Metazoa; Chordata; Gracilata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 3795)
Tardik, P.M.
Patent: WO 00/0945-A 5 (40-NV-2000);
Karolinska Innovations AB (SE)
FEATURES
Source
1..3795
BASE COUNT      1071 a      867 c      779 g      1078 t
ORIGIN
Alignment Scores:
Pred. No.:      5 556-84      Length:      3795
Score:          956.50      Matches:      168
Percent Similarity: 71.58%      Conservative: 36
Best Local Similarity: 58.95%      Mismatches: 78
Query Match:    57.93%      Indels:      3
Db:             6      Gaps:      1
US-09-624-670-64 (1-299) x AX052773 (1-3795)
QY      1 MetGluHspheaspIasSerLeuSerThrTyPheYalaPheLeuGlyProArgSP 20
DB      46 CTGAAGGCGTTGGATATGACATGCAATGCTTCTGGACACATGTTTGAACGAGAT 105
QY      21 ThrArgValIysGlyTrpPheLeuLeuAspAsnTyrlleProthPheValCysSerVal 40
DB      106 TTCGAGATTGCGGAGTGGTCTGCGGACTCTTACCTCCGCACTTATCTTACCATC 165
QY      41 lletyrleuLeuValItrPheuglyProlystYrMetLysAsnArgGlnProPheSer 60
DB      166 ACGTACCTGCTCGATATGCGGCTGGAACACATCATCAAGACAGCGCTGCTGCT 225
QY      61 CysArgGlyIleLeuGlnLeuTyfAsnLeuGlyLeuThLeuLeuSerLeuTyfMetPhe 80
DB      226 CTAGAGAGCATGCTACATGTATAACTTGAATTAATTAATTTTTPAATATATG 285
QY      81 TyrcIleuValItrGlyValItrPgluclyLysfyrAsnphPheGcysGlnGlythrArg 100

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Q3 178 ValLeuMetIysSerTyrTyrGlyLeuSerSerIleProSerMetArgProTyrLeuTrp 197
Dt .....
Q3 625 ATTCTTATGTAAGTCTGACATAGGACCTTCTGCTTTCCATGCTATGCAACAGTATCTTTGG 684
Dt .....
Q3 198 TTPLySLySTyrIleThrGlnGlyGlnLeuValGlnPheValLeuThrIleGlnThr 217
Dt .....
Q3 685 TGGAGAGAAATATCTCTACACAGGCTCAGCTGCTGAGATTGCTGCTCAGCATCAGCGACACG 744
Dt .....
Q3 218 ThrcysGlyValPheTrpProCysSerPheProLeuGlyTyrPheuphePheGlnIleGly 237
Dt .....
Q3 745 ATGAGCGCGCTGCGAAGCGTGTGGCTTCCCTTCGGTTCGTCATCTTCACATGTCATCT 804
Dt .....
Q3 238 TyrMetIleSerLeuIleAlaLeuPheThrAsnPheTyrIleGlnThrTyrAsnLys 257
Dt .....
Q3 805 TATATGCTTAAGCTTCAACCTCTCTTAAATTTTATGTTGACAGACATCGGAAAAAG 864
Dt .....
Q3 258 GlyAlaSerArgArgLysAspHisIleuLysGlyHisGlnAsnGlySerValAlaIleVal 277
Dt .....
Q3 865 -----CCAAATGAGAGAAAGTATGCAAGGCGCCTGCGAGGAGAAAGAAATGAA3----- 912
Dt .....
Q3 278 AsnGlyHisThrAsnSerPheProSerLeuGluAsnSerValLysProArgLys 295
Dt .....
Q3 913 AATGGTTTTTCCAAAGCTTACTTTCATCTTGACCAATGAGAGTGAATGACACAGAA 966
Dt .....
```

Search completed: June 15, 2003, 23:02:03
Job time : 2225.45 secs



GenCore version 5.1.6
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OM protein - nucleic search, using frame plus p2n model

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Run On:      June 15, 2004  20:45:36 ; Search time 209.16 Seconds
              (without alignments)
              3262 086 Million cell updates/sec
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Title: US-09-624-670-64
 Perfect score: 1651
 Sequence: I MEHFQASLSTYFKAFIGPPD... HTNSPSPLENSVKPRKQRD 299

Scoring table: BLOSUM62

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Ygapop	10.0
Fgapop	6.0
Delpop	6.0
Xgapext	0.5
Ygapext	0.5
Fgapext	7.0
Delext	7.0

Searched · 2185239 seqs, 1:25:09.159 residues

Total number of hits satisfying chosen parameters: 4370478

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NEW YORK 17, N.Y.

Maximum DB seq	length: 200000000
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Post-processing - Minimum March 08

Maximum Match 100

Listing first 45 summaries

Command line parameters.

[illegible]

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2:	/SID52/qcdata/qcneseq/geneseq-emb1/NA1981.DAT.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	%			DB	ID	Description
			Match	Length	Count			
1	1651	100.0	900	24	ARK46370	Mouse elongase MEL		
2	1523	94.4	914	21	AAK34241	Human elongase HSE		
3	1556	94.4	2001	23	AAK23421	Human prostate exp		
4	1556	94.4	2001	23	ABV24778	Human prostate exp		
5	1556	94.4	2001	23	ABV25364	Human prostate exp		
6	1559	94.4	2001	23	AAK29278	Human prostate exp		
7	1559	94.4	2313	21	AAK264369	Human vesicle asso		
8	1559	94.4	2627	22	AAK94330	Human full-length		
9	1559	94.4	2769	22	AAK44747	Human full-length		
10	1559	94.4	3083	22	AAK44919	Human contig poly		
11	1558	94.4	914	24	AAK46367	Human elongase HSE		
12	1555	94.2	2710	9	AAK54132	Breast cancer prot		
13	1489.5	90.2	3571	9	AAN81168	Fragment from clon		
14	134.5	81.3	1957	24	AHU90474	Human polynucleot		
15	1148	69.5	975	22	AAK07290	Human cold-induced		
16	1108	67.1	871	22	AAK27318	CDNA encoding nove		
17	1085	65.7	680	22	AAK91444	Human CDNA 5'-end		
18	1085	65.7	680	22	AAK93349	Human CDNA clone r		
19	1069	64.7	748	22	AAK27317	CDNA encoding nove		
20	956.5	57.9	879	24	AAK46369	Mouse fatty acid e		
21	956.5	57.9	879	22	AAK31702	Mouse fatty acid e		
22	956	57.9	817	22	AAK93682	Human CDNA clone r		
23	954.5	57.8	3645	23	ABV242609	Human prostate exp		
24	954.5	57.8	3645	23	ABV24286	Human prostate exp		
25	954.5	57.8	3645	23	ABV28431	Human prostate exp		
26	772	46.8	809	22	AA197437	Human neuroblastom		
27	756	45.8	795	23	AAK95737	Human neuroblastom		
28	755	45.5	927	23	AAK93155	Human CDNA clone r		
29	724	43.7	1225	31	AAK77854	Human cancer assoc		
30	669	40.5	1292	24	AAK19307	Mouse elongation o		
31	654.5	39.6	972	24	AAK19305	Mouse elongation o		
32	653.5	39.6	1203	23	AAK91595	Human elongation o		
33	653.5	39.6	3383	24	AAK072496	DNA encoding novel		
34	653.5	39.6	2415	24	ABK28654	Human MDDT encodin		
35	624.5	37.8	493	24	ABQ01412	Human colon cancer		
36	624.5	37.8	967	24	AAK19105	Human elongation o		
37	598	36.2	874	22	AAK19105	Human CDNA 5'-end		
38	598	36.2	2090	22	AAK93947	Human CDNA clone r		
39	598	36.2	2090	22	AAK94230	Human full-length		
40	579	35.1	488	23	AAK76145	DNA encoding novel		
41	559	33.9	404	23	ABV07448	Human prostate exp		
42	552	33.9	598	23	ABV37362	Human prostate exp		
43	526	41.9	323	23	ABV08363	Human prostate exp		
44	526	31.9	363	23	ABK38270	Human prostate exp		
45	504	30.5	1914	23	ABL15699	Drosophila melanop		

ALIGNMENTS

RESULT 1
ABK46370
ID ABK46370 standard. CDNA: 900 BP.

XX
AC ABK46370-

XX 05-JUN-2002 (first entry)

XX
DE
Mouse elongase MFL07 cDNA

ss, yenc, elongate, polyunsaturated fatty acid, pufa, transgenic plant;
transgenic non human animal, plant oil, arachidonic acid, nutritional;
pharmaceutical, cosmetic, animal feed, testosterone, angioplasty, AIDS;
acquired immunodeficiency syndrome, multiple sclerosis, cachexia, asthma;
inflammatory skin disease, osteoporosis, kidney stone, cancer, eczema;
infectious arthritis, psoriasis, platelet aggregation;
vasodilation; cholesterol reduction, gastrointestinal bleeding.

OS Mus sp.
 PN W020208421 A2.
 XX
 PD 41-JAN 2002.
 XX
 PF 24-JUL-2001: 2001W0 US23259.
 XX
 PR 24-JUL-2000: 2000US 0644670.
 PR 11-JUL-2001: 2001US 0903456.
 XX
 PA (ABHO) ABHOTT LAB.
 PI Mukerji P, Das I, Huang Y, Parker-Harries JM, Leonard AF;
 PI Thurmond J, Pereira SL;
 XX WPI: 2002 17201722.
 DR P-PSDB: AA087834.
 XX
 PT Isolated nucleic acid sequences encoding elongase proteins, useful in
 PT the production of polyunsaturated fatty acids, e.g. arachidonic acid,
 PT which can then be used nutritional compositions and pharmaceutical
 PT compositions (for treating AIDS).
 XX
 PS Claim 8; Fig 58; 27pp; English
 XX
 CC The invention relates to isolated nucleic acid sequences encoding
 CC elongase proteins and the elongase proteins themselves. Also
 CC included are a purified polypeptide which elongates polyunsaturated
 CC fatty acids and has at least 30% amino acid similarity to the amino acid
 CC sequence to an elongase protein, a vector comprising the nucleic
 CC acid, a plant cell (or tissue or whole plant) comprising the vector and
 CC expressing the nucleic acid, a plant oil or acid expressed by the
 CC transgenic plant, and a transgenic non-human animal expressing elongase
 CC in its fluid. The nucleic acids and elongase proteins may be used
 CC directly or indirectly in the production of polyunsaturated fatty acids
 CC (pufa), for e.g. arachidonic acid, which can then be used nutritional
 CC compositions, pharmaceutical compositions, cosmetics and animal feeds.
 CC The pharmaceutical compositions may be used in the treatment of
 CC restenosis after angioplasty, AIDS (acquired immunodeficiency syndrome),
 CC multiple sclerosis, inflammatory skin diseases, osteoporosis, kidney or
 CC urinary tract stones, malignant cancer, cachexia associated with cancer,
 CC eczema, symptoms of inflammation, rheumatoid arthritis, asthma and
 CC psoriasis, they are also useful for inhibiting platelet aggregation,
 CC inducing vasodilation, reducing cholesterol, reducing or preventing
 CC gastrointestinal bleeding and side effects of non-steroidal
 CC anti-inflammatory drugs. The present sequence encodes an elongase
 CC of the invention.
 XX
 SQ Sequence 909 BP, 289 A, 256 C, 203 G, 235 T, 0 other.

Alignment Scores:
 Pred. No.: 5,574 171 Length: 900
 Score: 1651.00 Matches: 299
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 24 Gaps: 0

US 09-624 670 64 (1-299) x AR4476 (1 900)
 QY 1 MotGluHisPheAspAlaSerLeuSerThrTyrPheLysAlaPheGlyProArgAsp 20
 DB 1 ATGGAAATTTCGATGTCACACAGTACATATTTCAAGAGCTTCGAGGACGAGAT 60
 QY 21 ThrArgValLysGlyTyrPheLeuLeuAspAsnTyrIleGlyThrPheValCysSerVal 40
 DB 61 ACAAGATCAAGAGCATGCTCTCTCCCTGGACAAATATATCCCTACCGTTCTGTCGTT 120
 QY 41 IleTyrLeuLeuIleValTyrLeuGlyTyrProLysTyrMetLysAsnLysProPheSer 60
 DB 121 ATTACTACTCAATGATGAGTGGGACCAAAATATATGAAGACATGCTACCGTTCTCT 180

QY 61 CysArgGlyIleLeuGlnLeuGlyTyrAspGluGlyLeuThrLeuGluSerLeuTyrMetPhe 80
 DB 161 TGGGAGGATGAGAGTGGATGATAAGTTGGACTATGCTGTGTGTATATATGTTG 240
 QY 81 TyrGluLeuValThrGlyValTyrGluGlyLysTyrAsnPhePheCysIleGlyThrArg 100
 DB 241 TATCAGTTGGTGAACAGTGTGGAGAGGAAATAAATAATTTCTGCAACAGACG 300
 QY 101 SerAlaGlyGluSerAspMetLysIleIleArgValLeuTyrTyrTyrPheSerLys 120
 DB 301 AGGAGGAGAGATGAGATGATGAGATGAGAGTATGAGGATGATGAGTATATTTCCAAA 460
 QY 121 LeuIleGluPheMetAspThrPhePhePheIleLeuArgLysAsnAsnHisGlnIleThr 140
 DB 361 CTATGCAATTCATGACACACTTTTCTTCATGCTTGGCAAGAAATAATATATATATAT 420
 QY 141 ValIleHisValTyrHisIleAlaThrMetLeuAsnIleTyrTyrPheValMetAsnTrp 160
 DB 421 GTGCTGCATGCTACCAACCACTACCACTGCTCAATATCTGTGCTTGTGACAACTCG 480
 QY 161 ValProCysGlyHisSerTyrPheGlyAlaThrLeuAsnSerPheIleHisValLeuMet 180
 DB 481 GTTCATGAGGACAAATATATATTTGGTGGCAACTATACAGATTTATCATGCTCTCATG 540
 QY 181 TyrSerTyrTyrGlyLeuSerSerIleThrSerMetArgProLysIleThrTyrPheLys 200
 DB 541 TATCTGACTATGTCGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
 QY 201 TyrIleThrGluGlyGlnLeuValGlnPheValLeuThrIleIleGlnThrThrCysGly 220
 DB 601 TACATCACTCAAGGAGCTGGGCCAGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
 QY 221 ValPheTyrProCysSerPheProLeuGlyTyrLeuIlePheGluIleIleTyrMetIle 240
 DB 661 GTCTTCTGGGACAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
 QY 241 SerLeuAlaLeuPheThrAsnPheTyrIleGlnThrTyrAsnLysLysGlyAlaSer 260
 DB 721 TGGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
 QY 261 ArgArgAspAspHisLeuLysGlyHisGlnAsnGlySerValAlaIleValAsnGlyHis 280
 DB 781 CGGACCAAGACCACTTGAAGGGGCACTACAAATGGGCTGCTGCTGCTGCTGCTGCTGCT 840
 QY 281 ThrAsnSerPheProSerLeuGluAsnSerValLysProArgLysGluArgLysAsp 299
 DB 841 ACCAAGAGCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 897
 RESUL1 2
 AA294241
 ID AA294241 standard; cDNA 914 BP.
 AC
 AA294241
 DT 03-JUL-2000 (first entry)
 DE Human elongase HSELO1 cDNA.
 KW Elongase; HSELO1; polyunsaturated fatty acid; adipic acid;
 KW dihydro gamma linolenic acid; eicosatetraenoic acid;
 KW transgenic plant; transgenic animal; human; ss
 OS Homo sapiens.
 XX W0200012720 A2.
 XX 09-MAR-2000.
 XX 30-AUG-1999: 99W0-US14715.
 XX 02-SEP-1998: 98US-0145428.
 XX (ABHO) ABHOTT LAB.

XX Mukerji P, Leonard AE, Huang Y, Thurmond J, Kirchner SJ;
 PI Parker-Barnes JM, Das T;
 DR WPI: 2000-237881/20.
 XX P-PSDB: AAY83932.
 PI Isolated nucleic acids encoding elongase enzymes for producing
 PT polyunsaturated fatty acids that can be used to form nutritional
 PT compositions -
 XX Claim 114; Fig 43; 210pp; English.
 XX This sequence is the coding region of cDNA encoding a human
 CC elongase, termed HSELO1 (see AAY79244). The cDNA was isolated from a
 CC human liver cDNA library by PCR amplification (see AAY294253-54).
 CC HSELO1 is involved in the elongation of polyunsaturated fatty acids
 CC (PUFAs). It is capable of catalysing the conversion of
 CC gamma-linolenic acid, stearidonic acid and arachidonic acid to
 CC dihomogamma-linolenic acid, eicosatetraenoic acid and adrenic acid,
 CC respectively. The invention provides M. alpina, human and
 CC Caenorhabditis elegans elongase nucleotide sequences (see AAY294239-41)
 CC and proteins, vectors comprising nucleotide sequences, eukaryotic
 CC and prokaryotic host cells, plant cells, plants or plant tissues
 CC comprising such vectors, transgenic non-human mammals whose genome
 CC comprises a nucleotide sequence encoding an elongase, a method for
 CC producing a PUFA using a host cell expressing an elongase, and
 CC nutritional, pharmaceutical, cosmetic and animal feed compositions
 CC comprising the PUFA.
 XX
 SQ Sequence 914 BP; 237 A, 223 C, 199 G; 255 T; 0 other;
 Alignment Scores:
 Pred. No.: 6 69e-161 Length: 914
 Score: 1559.00 Matches: 278
 Percent Similarity: 97.32% Conservativity: 13
 Best Local Similarity: 92.98% Mismatches: 8
 Query Match: 94.43% Indels: 0
 DB: 21 Gaps: 0

US-09-624 670-64 (1-299) x AAY294241 (1-914)

QY 1 MetGluHisPheAspAlaSerLeuSerThrTyrPheLysAlaPheLeuGlyProArgAsp 20
 DB 1 ATGGACATTTTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 60
 QY 21 ThrArgValLysGlyTyrPheLeuLeuAspAsnTyrIlePheCysVal 40
 DB 61 ACTAGAGTAAAGCAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 120
 QY 41 IleTyrLeuLeuValTyrPheLeuGlyProLysTyrMetLysAsnArgGlnProPheSer 60
 DB 121 ATATATTACATATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
 QY 61 CysArgGlyIleLeuGlnLeuTyrAsnLeuGlyLeuThrLeuLeuSerLeuTyrMetPhe 80
 DB 181 TGGCGGGGATTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
 QY 81 TyrGluLeuValThrGlyValTyrGlyValTyrGlyValTyrGlyValTyrGlyVal 100
 DB 241 TGTGAGTTAGTAAACAGGAGTATGGCAAGGCAAAATACAACTTCTTCTGTCAGGGCACAC 300
 QY 101 SerAlaGlyGluSerAspMetLysIleIleArgValLeuTyrTrpTyrTrpPheSerLys 120
 DB 301 ACCGCGAGGAGATCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
 QY 121 LeuIleGluPheMetAspThrPhePheIleLeuArgLysAsnAsnHisGlnIleThr 140
 DB 361 CTCATAGATTTATGAAATTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 420
 QY 141 ValLeuHisValTyrHisHisAlaThrMetLeuAsnIleTyrTrpPheValMetAsnTrp 160
 DB 421 GTCTGTCAGCTTACACCATGCCCTCGATGCTGACATCTGCTGCTGCTGCTGCTGCTGCTG 480

QY 161 ValProCysGlyHisSerTyrPheGlyAlaThrLeuAsnSerPheIleHisValLeuMet 180
 DB 481 GTCCCTGGCCGACCTCTTATTTTGGTGCACACTAATAGCTTCATCCAGTCTCTCATG 540
 QY 181 TysSerTyrTyrGlyLeuSerSerIleProSerMetArgProTyrTyrTrpTyrLys 200
 DB 541 TACTCTTACTATGTTTGTGTCAGTCCCTTCATCGCTCCATACCTCTGTGGTGAAGAAG 600
 QY 201 TyrIleThrGlnGlyGlnLeuValGlnPheValLeuThrIleIleLeuThrThrCysGly 220
 DB 601 TACATCACTCAGGGGAGCTGCTTCACTTGTCTGACAAATCATCCAGACCAAGCTCGGG 660
 QY 221 ValPheTrpProCysSerPhePheLeuGlyTyrPhePheGlnIleGlyTyrMetIle 240
 DB 661 GTCATCTGGCGGTGCACATTCCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 720
 QY 241 SerLeuIleAlaLeuPheThrAsnPheTyrIleGlnThrTyrAsnLysLysGlyAlaSer 260
 DB 721 TCCCTGATGCTCTCTTCACAACTTCTACATTCACACCTACACCAAGAAAGGGCCTCC 780
 QY 261 ArgThrLysAspHisLeuLysGlyHisGlnAsnGlySerValAlaAlaValAsnGlyHis 280
 DB 781 CCAAGGAAAGACACCTGGAAGGACCCAGATGGGTTCATGCTGCTGCTGCTGCTGCTGCT 840
 QY 281 ThrAsnSerPheProSerLeuGluAsnSerValLysProArgLysGlnArgLysAsp 299
 DB 841 ACCAACACGCTTTTCACCCCTGGAAAGCAATGTGAAGCCAAAGGAAGCTCGGAAGGAT 897

RESULT 3
 ABV23421
 ID ABV23421 standard; cDNA; 2001 BP.
 XX AC ABV23421;
 XX DT 16-SEP-2002 (first entry)
 XX DE Human prostate expression marker cDNA 23412.
 XX KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
 XX OS Homo sapiens.
 XX PN WO200160860-A2.
 XX PD 23-AUG-2001.
 XX PF 20-FEB-2001; 2001WO-US05171.
 XX PR 17-FEB-2000; 2000US-183319P.
 XX PR 16-MAR-2000; 2000US-189862P.
 XX PR 25-MAY-2000; 2000US-207454P.
 XX PR 09-JUN-2000; 2000US-211314P.
 XX PR 18-JUL-2000; 2000US-216007P.
 XX PR 13-DEC-2000; 2000US-255281P.
 XX PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 XX PI Schlegel R, Endege WO, Monahan JE;
 XX DR WPI: 2001-662795/76.
 XX Novel isolated nucleic acid molecule associated with cancerous state of
 PT prostate cells and correlating with presence of prostate cancer, useful
 PT for detecting presence of prostate cancer, stage of prostate cancer -
 PS Claim 1; Page 4265-4266; 11750pp; English.
 CC The invention relates to an isolated nucleic acid molecule (1) comprising
 CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
 CC specification or its complement. (1) is useful for:
 CC (a) assessing whether a patient is afflicted with prostate cancer;

CC	(b) monitoring the progression of prostate cancer in a patient;
CC	(c) assessing the efficacy of a test compound to inhibit prostate
CC	cancer in a patient;
CC	(d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC	in a patient;
CC	(e) selecting a composition for inhibiting prostate cancer in a patient;
CC	(f) assessing the prostate cell carcinogenic potential of a compound;
CC	(g) determining whether prostate cancer has metastasized in a patient;
CC	(h) assessing the aggressiveness or indolence of prostate cancer in a
CC	patient;
CC	(i) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX	
XX	Sequence: 2001 RP; 527 A; 541 G; 499 G; 489 T; 5 other;

US-09-624-670 64 (1-299) x ABV23421 (1-2001)

QY	1	MetGluHisPheAspAlaSerLeuSerThrTyrPheLeuAlaPheLeuGlyProArgAsp	20
DB	177	ATGGAAACATTTTGATGATACACTTATATATATTTTAAAGGATATGATAGGATATATAT	206
QY	21	ThrArgValLysGlyTyrPheLeuLeuAspAsuTyrLLePrlThrPheValCysSerVal	40
DB	237	ACTACAGTAAAGCAAGCTTCTCTCTGCGCAAAATATATACCAACATTTATCTGCTCTGCTG	296
QY	41	IleTyrLeuLeuIleValIrpLeuGlyProLysTyrMetLysAsnArgGlnProPheSer	60
DB	247	ATATATTTTAAATGTATGATGCTGGACCAAAAAATATAGAGAAATAAAACAGCATTCCT	456
QY	61	CysArgGlyIleLeuGlnLeuLeuTyrAsnLeuGlyLeuThrLeuLeuSerLeuIleThrMetPhe	80
DB	357	TGCGGGGCAATTTTAGTGTGCTATAGCACTTGGACTTACACTGTGCTCTGTATATGTTCT	416
QY	81	TyrGluLeuValThrGlyValIrpGlnGlyLysTyrAsnPhePheCysIleGlyThrArg	100
DB	417	TGTCACTTATTAACAGACAGTATGGCAAGCAAAATACAACTTCTCTGTCAGGCGCACAGC	476
QY	101	SerAlaGlyHisSerAspMetCysIleIleArgValLeuIrpTrpTyrTyrPheSerCys	120
DB	477	ACGCACAGCAAT	536
QY	121	LeuIleGluPheMetAspThrPhePhePheIleLeuArgLysAsnAsnHisGlnIleThr	140
DB	537	CTCATASAAATTTATGACAAATTTCTCTTCTATCTGATGATGATGATGATGATGATGATGAT	596
QY	141	ValLeuIleValTyrHisHisAlaThrMetLeuAsnIleIrpTrpPheValMetAsnTrp	160
DB	597	GTCCTGCACGCTACACAAACGCTGCACTGCAACATCGGAGGTTTGTGATGAGCACTGG	656
QY	161	ValProCysGlyHisSerTyrPheGlyValThrLeuAsnSerPheIleHisValLeuMet	180
DB	657	GTCCGCTCGCGCACCTGATTTTGTGTGCACAACTTAATAGCTTCAACCAATGCTGCAATG	716
QY	181	TyrSerTyrTrpGlyLeuSerSerIlePheSerMetArgPheGlyLeuIrpTrpLys	200
DB	717	TACTCTACTATGTTTGTGTAGGCGGCTTGTATATATATATATATATATATATATATATATAT	776
QY	201	TyrIleThrGlnGlyIleLeuValGlnPheValLeuThrIleIleGlnThrTyrCysGly	220
DB	777	TACATCACTAAGCGCAATGCTCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	836
QY	221	ValPheTrpProCysSerPheProLeuGlyTyrLeuPhePheGlnIleGlyTyrMetIle	240
DB	847	GTATCTAGAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	896
QY	241	SerLeuAlaAlaLeuPheThrAsnPheTyrIleGlnThrTyrAsnHisValIleValSer	260

Best Local Similarity: 92.98% Mismatches: 8
 Query Match: 94.43% Indels: 0
 DB: 23 Gaps: 0

US-09-624-670-64 (1-299) x ABV24778 (1-2001)

QY 1 MetGluHisPheAspAlaSerLeuSerThrTyrPheLysAlaPheLeuGlyProArgAsp 20
 DB 177 ATGGAACATTTTGCATGACATCTTAGTACCTATTTCAGGCATGTTAGGCTCGAGAT 236
 QY 21 ThrArgValLysGlyTyrPheLeuLeuAspAsnTyrIleProThrPheValCysSerVal 40
 DB 237 ACTAGAGTAAAGGATGCTTCTTCTGGACAATTATATACCCACATTTATCTGCTGTC 296
 QY 41 IleTyrLeuLeuLeuValTyrPheLeuGlyProLysTyrMetLysAsnArgGlnProPheSer 60
 DB 297 ATATATTACTAATTTCTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 256
 QY 61 CysArgGlyIleLeuGlnLeuTyrAsnLeuGlyLeuThrLeuLeuSerLeuTyrMetPhe 80
 DB 357 TCCCGGGGATTTAGTGGTGTATTAACCTGGACTCACACTGCTGCTGCTGCTGCTGCTGCT 416
 QY 81 TyrGluLeuValThrGlyValTyrPheGlyLysTyrAsnPhePheCysGlnGlyThrArg 100
 DB 417 TGTGAGTTAGTAACAGGAGTATGGGAGCGCAATACAACTTCTTCTGCTGCTGCTGCTGCTGCT 476
 QY 101 SerAlaGlyGluSerAspMetLysIleIleArgValLeuTyrPheSerLys 120
 DB 477 ACCGAGGAGATCAGATATGAGATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 536
 QY 121 LeuIleGluPheMetAspThrPhePheIleLeuArgLysAsnAsnHisGlnIleThr 140
 DB 537 CTCATAGAAATTTATGACATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 596
 QY 141 ValLeuHisValTyrHisAlaThrMetLeuAsnIleTyrPheValMetAsnTrp 160
 DB 597 GTCCCTCCACGCTACACACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 656
 QY 161 ValProCysGlyHisSerTyrPheGlyAlaThrLeuAsnSerPheIleHisValLeuMet 180
 DB 657 GTCCCTCCACGCTACACACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 716
 QY 181 TyrSerTyrTyrGlyLeuSerSerIleProSerMetArgProTyrLeuTyrPheLysLys 200
 DB 717 TACTCTTACTATGTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 776
 QY 201 TyrIleThrGlnGlnLeuValGlnPheValLeuThrIleIleGlnThrThrCysGly 220
 DB 777 TACATCCTCAGGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 836
 QY 221 ValPheTrpProCysSerPheProLeuGlyTyrPheGlnIleGlyTyrMetIle 240
 DB 837 GTCACTGGCGGTGATCATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 896
 QY 241 SerLeuIleAlaLeuPheThrAsnPheTyrIleGlnThrTyrAsnLysGlyAlaSer 260
 DB 897 TCTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 956
 QY 261 ArgArgLysAspHisLeuLysGlyHisGlnAsnGlySerValAlaAlaValAsnGlyHis 280
 DB 957 CCAAGGAAGACACCTCAAGGACACCAAGATGGTCCATGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1016
 QY 281 ThrAsnSerPheProSerLeuGluAsnSerValLysProArgLysGlnArgLysAsp 299
 DB 1017 ACCACAGCTTTTTCACCTGCAAAACAAATGTGAAGCCAGCAAGCTGCGGAAGGAT 1073

RESULT 5
 ABV25364
 ID ABV25364
 XX standard; cDNA; 2001 BP.
 AC
 XX ABV25364;
 AC
 DT 16-SEP-2002 (first entry)

XX Human prostate expression marker cDNA 25355.
 DF Human, prostate cancer, cytostatic; carcinogen, pharmacodynamic marker.
 KW pharmacogenomic marker; gene; ss.
 KW Homo sapiens.
 OS Homo sapiens.
 PN WC200160860-A2.
 FD 23-AUG-2001.
 XX 20-FEB-2001; 2001WO-US05171.
 XX 17-FEB-2000; 2000US-183319P.
 PP 16-MAY-2000; 2000US-180862P.
 PP 25-MAY-2000; 2000US-207454P.
 PP 09-JUN-2000; 2000US-211314P.
 PP 18-JUL-2000; 2000US-216007P.
 PP 13-DEC-2000; 2000US-255281P.
 XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 PA Schlegel R, Endege WO, Monahan JE;
 PI WPI; 2001-662795/76.
 DR Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer -
 XX Claim 1; Page 5005-5006; 11750pp; English.
 XX The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:
 CC (a) assessing whether a patient is afflicted with prostate cancer;
 CC (b) monitoring the progression of prostate cancer in a patient;
 CC (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
 CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;
 CC (f) assessing the prostate cell carcinogenic potential of a compound;
 CC (g) determining whether prostate cancer has metastasized in a patient;
 CC (h) assessing the aggressiveness or indolence of prostate cancer in a patient;
 CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker.
 SQ Sequence 2001 BP; 527 A; 581 C; 399 G; 489 T; 5 other;

Alignment Scores:
 Pred. No.: 2,02e-160 Length: 2001
 Score: 1559.00 Matches: 278
 Percent Similarity: 97.32% Conservative: 13
 Best Local Similarity: 92.98% Mismatches: 8
 Query Match: 94.43% Indels: 0
 DB: 23 Gaps: 0

US-09-624-670-64 (1-299) x ABV25364 (1-2001)

QY 1 MetGluHisPheAspAlaSerLeuSerThrTyrPheLysAlaPheLeuGlyProArgAsp 20
 DB 177 ATGGAACATTTTGCATGACATCTTAGTACCTATTTCAGGCATGTTAGGCTCGAGAT 236
 QY 21 ThrArgValLysGlyTyrPheLeuLeuAspAsnTyrIleProThrPheValCysSerVal 40
 DB 237 ACTAGAGTAAAGGATGCTTCTTCTGGACAATTATATACCCACATTTATCTGCTGTC 296
 QY 41 IleTyrLeuLeuLeuValTyrPheLeuGlyProLysTyrMetLysAsnArgGlnProPheSer 60
 DB 297 ATATATTACTAATTTCTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 356

XX DE Human full-length polynucleotide sequence #172.
 XX KW Mammal; human; rhesus monkey; baker's yeast; fission yeast; Norway rat;
 XX KW mouse; Chinese hamster; African clawed frog; fruit fly; dog; leukaemia;
 XX KW cancer; lymphoma; neuroblastoma; autoimmune disorder; cell proliferation;
 XX KW nervous system disorder; inflammatory disorder; cell differentiation; ds;
 XX KW aneuploidy; stem cell growth factor; activin; inhibin; cartilage; burn;
 XX KW genetic disorder; bone regeneration; tendon; ligament; tissue repair;
 XX KW cytostatic; antirheumatic; antiarthritic; vulnery; antiinflammatory;
 XX KW antibacterial; immunosuppressive; vasotropic; antiparkinsonian;
 XX KW neuroprotective; osteopathic; antidiabetic; antiallergic;
 XX KW immunostimulant; analgesic; gene therapy.
 XX OS Homo sapiens.
 XX PN WO200164834-A2.
 XX PD 07-SEP-2001
 XX PF 26-FEB-2001, 2003WO US04926.
 XX PR 28-FEB-2000; 2000US 0515126.
 XX PP 18-MAY-2000; 2000US 0577409.
 XX PR 17-JUN-2000; 2000US 0597707.
 XX PR 14-JUL-2000; 2000US 0616807.
 XX PR 19-SEP-2000; 2000US 0664641.
 XX PA (HYSK-) HYSK INC.
 XX PI Tanq YT, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F;
 XX PI Xue AJ, Yang Y, Wehrman T, Wang J, Ma Y, Wang D, Chen R, Xu C;
 XX PI Brnmanac R;
 XX WI: 2001-589862/66.
 XX P:PSDB: AA027847.
 XX PT Novel polypeptides and nucleic acids obtained from cDNA libraries
 XX PT prepared from various human tissues, for diagnosis, treatment of
 XX PT cancer, neurological, inflammatory disorders and for use in arrays for
 XX PT detection -
 XX PS Claim 1, SEQ ID NO 172, 153pp, English.
 XX CC Sequences AAS44576-AAS44919 represent full-length polynucleotides and
 XX CC contig polynucleotides encoding polypeptides of the invention. The DNA
 XX CC and protein sequences are useful for the treatment, diagnosis and
 XX CC prevention of various types of disorder in a mammalian subject such as a
 XX CC human, dog, monkey, mouse, hamster or rat. The disorders include cancers
 XX CC such as leukaemia, lymphoma and neuroblastoma, autoimmune disorders such
 XX CC as multiple sclerosis, connective tissue disease, rheumatoid arthritis,
 XX CC diabetes mellitus, allergic rhinitis, asthma and eczema, nervous system
 XX CC disorders such as Parkinson's disease, Alzheimer's disease, Huntington's
 XX CC chorea, amyotrophic lateral sclerosis, spinal muscular atrophy and
 XX CC Wernerke disease, inflammatory disorders such as hepatitis, Crohn's
 XX CC disease, ischaemia-reperfusion injury, shock, sepsis and inflammatory
 XX CC bowel disease. The sequences exhibit activity relating to angiogenesis,
 XX CC cell proliferation, cell differentiation, stem cell growth factor,
 XX CC activin or inhibin. Therefore, they can be used to manipulate stem cells
 XX CC in culture to give rise to neuroepithelial cells that can be used to
 XX CC augment or replace cells damaged by illness, accidental damage or genetic
 XX CC disorders. The sequences may also be used for regeneration of bone,
 XX CC cartilage, tendons and ligaments and in tissue repair and burn healing
 XX CC Note. Some sequences for this patent did not form part of the printed
 XX CC specification, but were obtained in electronic format directly from Wipo
 XX CC at http://wipo.int/pub/published_pct_sequences.
 XX SQ Sequence 276a BP, 799 A, 543 C, 554 G, 873 T, 0 other;
 Alignment Scores:
 Pred. No.: 3,180-160 Length: 2769
 Score: 1559.00 Matches: 278
 Percent Similarity: 97.32% Conservative: 13

Best Local Similarity: 92.98% Mismatches: 8
 Query Match: 94.43% Indels: 0
 DB: 22 Gaps: 0
 US-09-624-670-64 (1-299) X AAS44747 (1-2769)
 QY 1 MetGluHisPheAspAlaSerLeuSerThrTyrPheLysAlaPheLeuGlyProArgAsp 20
 DB 136 ATGGAAACATTTGATGCACTACCTAGTACCTATTTCAAGGCACTTGTAGGCCCTCGAGAT 195
 QY 21 ThrArgValLysGlyTyrPheLeuLeuAspAsnTyrTleProThrPheValCysSerVal 40
 DB 196 ACTAGAGTAAAGGATGTTCTTCTGGACAATTATATACCCACATTTATCTGCTGCTGTC 255
 QY 41 TleTyrLeuLeuLeuValTyrPheGlyProLysTyrMetLysAsnArgGlnProPheSer 60
 DB 256 ATATATTTTACTAATTGTATGCTGGACCAAAATACATGAGGAAATAAACACACCATCTCT 315
 QY 61 CysArgGlyLleLeuGlnLeuTyrAsnLeuGlyLeuThrLeuLeuSerLeuTyrMetPhe 80
 DB 316 TGTGGGGGGAATTTAGTGTGTATTAACCTTGGACTCAGATCGCTCTCTGTATATGTTTC 375
 QY 81 TyrGluLeuValLleGlyValLlePheGlyLysTyrAsnPhePheCysGlnGlyThrArg 100
 DB 376 TGTGATTTAGTAAACAAAGATATGGAAGGCAAAATACAACTTCTTCTGTAGGGCACACGC 435
 QY 101 SerAlaGlyGlySerAspMetLysLleLleArgValLeuTyrPheTyrPheSerLys 120
 DB 436 ACCGGCAGGAGAAATCAGATATCAAGATTAACGCTGCTGCTGCTGCTGCTGCTGCTGCTG 495
 QY 121 LeuLleGluPheMetAspThrPhePhePheLleLeuArgLysAsnAsnHisGlnIleThr 140
 DB 496 CTGATAGAAATTTATGGACACTTCTTCTTCTATCTGCGCAAGAAACACACACATCAGC 555
 QY 141 ValLeuHisValTyrHisHisAlaThrMetLeuAsnLleTyrPheValMetAsnTyr 160
 DB 556 GTCTGTGCACTGTACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 615
 QY 161 ValProCysGlyHisSerLysPheGlyAlaThrLeuAsnSerPheLleHisValLeuMet 180
 DB 616 GTCCCTCTGGGGCACTCTTATTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 675
 QY 181 TyrSerLysTyrGlyLeuSerSerLysPheProSerMetArgProTyrLeuTyrTrpLysLys 200
 DB 676 TACTCTTACTATGTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 735
 QY 201 TyrLleThrGlnGlnLeuValGlnPheValLeuThrLleLleGlnThrThrCysGly 220
 DB 736 TACATCACTCAAGGGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 795
 QY 221 ValPheTyrProCysSerPheProLeuGlyTyrPhePhePheGlnLleGlyTyrMetIle 240
 DB 796 GTTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 855
 QY 241 SerLeuLleAlaLeuPheThrAsnPheTyrLleGlnThrTyrAsnLysLysGlyAlaSer 260
 DB 856 TCCCTGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 915
 QY 261 ArgArgLysAspHisLeuLysGlyHisGlnAsnGlySerValAlaAlaValAsnGlyHis 280
 DB 916 CGAAGGAAAGACACACCTGAAAGGACACACAGATGAGGTCATGCTGCTGCTGCTGCTGCTG 975
 QY 281 ThrAsnSerPheProSerSerLeuGluAsnSerValLysTyrProArgLysGlnArgLysAsp 299
 DB 976 ACCCAACAGTTTTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1032
 RESULT 10
 AAS44919
 ID AAS44919 standard; DNA: 3083 BP.
 XX AC AAS44919;
 XX DT 18-DEC-2001 (first entry)

Human contig polynucleotide sequence #172.

Mammal; human; chesun monkey; baker's yeast; fission yeast; Norway rat; mouse; Chinese hamster; African clawed frog; fruit fly; dog; leukaemia; cancer; lymphoma; neuroblastoma; autoimmune disorder; cell proliferation; nervous system disorder; inflammatory disorder; cell differentiation; ds; angiogenesis; stem cell growth factor; activin; inhibin; cartilage; burn; genetic disorder; bone regeneration; tendon; ligament; tissue repair; cystic; antirheumatic; antiarthritic; vulnary; antiinflammatory; antibacterial; immunosuppressive; vasotropic; antiparkinsonian; neuroprotective; osteopathic; antidiabetic; antidiastmatic; antiallergic; immunostimulant; analgesic; gene therapy.

OS Homo sapiens.
 OS Synthetic.
 XX
 XX
 PN W0200164834-A2.
 PD
 PD 07-SEP-2001.
 XX
 XX
 XX 26-FEB-2001; 2001W0-0S04926.
 XX
 PR 28-FEB-2000; 2000US-0515136.
 PR 18-MAY-2000; 2000US-0577409.
 PR 17-JUN-2000; 2000US-0597707.
 PR 14-JUL-2000; 2000US-0616807.
 PR 19-SEP-2000; 2000US-0664641.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 P1 Tang YF, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F;
 P1 Xue AJ, Yang Y, Wehrman T, Wang J, Ma Y, Wang D, Chen R, Xu C;
 P1 Dmanac P;
 XX
 DR WPI: 2001-589862/66.
 DR P-PSDB; AAU28019.
 XX
 PT Novel polypeptides and nucleic acids obtained from cDNA libraries
 PT prepared from various human tissues, for diagnosis, treatment of
 PT cancer, neurological, inflammatory disorders and for use in arrays for
 PT detection
 XX
 PS Claim 1; SEQ ID NO 516; 15app; English.
 XX
 CC Sequences AA544576-AA544919 represent full-length polynucleotides and
 CC contig polynucleotides encoding polypeptides of the invention. The DNA
 CC and protein sequences are useful for the treatment, diagnosis and
 CC prevention of various types of disorder in a mammalian subject such as a
 CC human, dog, monkey, mouse, hamster or rat. The disorders include cancers
 CC such as leukaemia, lymphoma and neuroblastoma, autoimmune disorders such
 CC as multiple sclerosis, connective tissue disease, rheumatoid arthritis,
 CC diabetes mellitus, allergic rhinitis, asthma and eczema, nervous system
 CC disorders such as Parkinson's disease, Alzheimer's disease, Huntington's
 CC chorea, amyotrophic lateral sclerosis, spinal muscular atrophy and
 CC Werner's disease, inflammatory disorders such as nephritis, Crohn's
 CC disease, ischaemia reperfusion injury, shock, sepsis and inflammatory
 CC bowel disease. The sequences exhibit activity relating to angiogenesis,
 CC cell proliferation, cell differentiation, stem cell growth factor,
 CC activin or inhibin, therefore, they can be used to manipulate stem cells
 CC in culture to give rise to neuroepithelial cells that can be used to
 CC augment or replace cells damaged by illness, accidental damage or genetic
 CC disorders. The sequences may also be used for regeneration of bone,
 CC cartilage, tendons and ligaments and in tissue repair and burn healing.
 CC Note: Some sequences for this patent did not form part of the printed
 CC specification, but were obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 S0 Sequence 3083 BP; 884 A; 594 C; 607 G; 996 T; 2 other;

Alignment Scores:

Pred. No.: 3,7c 160 Length: 3083

Score: 1559.00 Matches: 278

Percent Similarity: 97.32% Conservat: 14
 Best Local Similarity: 92.98% Mismatches: 8
 Query Match: 94.43% Indels: 0
 Db: 22 Gaps: 0

US-09-624-670-64 (1-299) X AA544919 (1-3083)

QY 1 MetGluHisPheAspAlaSerLeuSerThrTyrPheValAlaPheLeuGlyProArgasp 20

DB 136 ATGAAATTTTGTATGATACACTAGTAAATTTTAAAGAAATGTTAGAGCTTACGAT 195

QY 21 ThrArgValIysGlyIrrPheLeuLeuAspAsnTyrLeuPhePheValCysSerVal 40

DB 196 ACTAGACTAAAGGCAATGTTCTTCTGGCAATTAATAATACATTAATCTGCTCTGTC 255

QY 41 IleTyrLeuLeuLeuValTrpLeuGlyProLysTyrMetLysAsuArgQinProPheSer 60

DB 256 ATATATTTACTAAATGATGGTGGGACCAAAATAATATGAGAAATAAAACAGCATTTCT 315

QY 61 CysArgGlyIleLeuGlnLeuTyrAsnLeuGlyLeuIrrLeuLeuSerLeuTyrMetPhe 80

DB 316 TGGAGAGGATTTTATGAGTATAAATCTGGACTTACATCTGCTGCTGTATATATGTC 475

QY 81 TyrGluLeuValThrGlyValTrpGluGlyLysTyrAsnPhePheCysGlnGlyIrrArg 100

DB 376 TGTCAAGTTAGTAACAGCAGTATGGCAAGCAAAATAAATCTGCTGCTGCTGCTGCTG 435

QY 101 SerAlaGlyGluSerAspMetLysIleLeuValLeuIrrTyrTyrTyrPheSerLys 120

DB 436 ACCGAGGAGAAATCATATGAGATTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 495

QY 121 LeuIleGluPheMetAspThrPhePhePheIleLeuArgLysAsuHisGlnIleThr 140

DB 496 CTCATAGAAATTTATGGACATTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 555

QY 141 ValLeuHisValTyrHisHisAlaThrMetLeuAsnIleIrrPhePheValMetAsnTrp 160

DB 556 GTCTGACAGCTTACCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 615

QY 161 ValProCysGlyHisSerTyrPheGlyAlaThrLeuAsuSerPheIleHisValLeuMet 180

DB 616 GTCCCTGCGGCGACTCTTATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 675

QY 181 TyrSerTyrTyrGlyLeuSerSerIleProSerMetArgProTyrLeuTrpTrpLys 200

DB 676 TACTCTTACTATGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 735

QY 201 TyrIleThrGlyGlnLeuValGlnPheValLeuIrrIleIleGlnIrrThrCysGly 220

DB 736 TACATCACAGGGGCGAGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 795

QY 221 ValPheTrpProCysSerPheProLeuGlyTrpLeuPhePheGlnIleIleTyrMetIle 240

DB 796 GTCACTGCGGCGTGGACATTTCCCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 855

QY 241 SerLeuIleAlaLeuPheThrAsnThrIleGlnIrrTyrAsnLysCysGlyAlaSer 260

DB 856 TCCCTGATTTGCTCTCTTACAAACTTCTACATTTAGAGCTAATACAGAAAGGGGCTCC 915

QY 261 ArgArgLysAspHisLeuLysGlyHisGlnAsnGlySerValAlaAlaValAsnGlyHis 280

DB 916 GTAAAGAAAGAAATCTTAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 975

QY 281 ThrAsaSerPheProSerLeuGluAsnSerValLysProArgLysGlnArgLysAsp 299

DB 976 ACCAAAGCTTTTACACCGCTGGCAAAATGCTGCTGCTGCTGCTGCTGCTGCTGCT 1042

RESULT 11

ABK46367

ID ABK46367 standard; cDNA: 914 BP.

XX

AC ABK46367;

XX

DT 05-JUN-2002 (first entry)
 XX Human elongase HSELO1 cDNA.
 KW ss: gene; elongase; polyunsaturated fatty acid; pufa; transgenic plant;
 KW transgenic non-human animal; plant oil; arachidonic acid; nutritional;
 KW pharmaceutical; cosmetic; animal feed; restenosis; angioplasty; AIDS;
 KW acquired immunodeficiency syndrome; multiple sclerosis; cachexia; asthma;
 KW inflammatory skin disease; osteoporosis; kidney stones; cancer; eczema;
 KW inflammation; rheumatoid arthritis; psoriasis; placental aggragation;
 KW vasodilation; cholesterol reduction; gastrointestinal bleeding.
 XX Homo sapiens.
 OS
 XX
 PN WO200208401-A2.
 PD
 XX 31-JAN-2002.
 XX
 PF 24-JUL-2001; 2001WO US3259.
 XX
 PR 24-JUL-2000; 2000US-0624579.
 PR 11-JUL-2001; 2001US-0903456.
 XX
 PA (ABBO) ABBOTT LAB.
 XX
 PI Mukerji P, Das T, Huang Y, Parker-Barnes JM, Leonard AE;
 PI Thurmond J, Pereira SL;
 XX
 DR WPI; 2002-172011/22.
 DR P-PSDB: AAU87830.
 XX
 PT Isolated nucleic acid sequences encoding elongase proteins, useful in
 PT the production of polyunsaturated fatty acids, e.g. arachidonic acid,
 PT which can then be used nutritional compositions and pharmaceutical
 PT compositions (for treating AIDS) -
 XX
 PS Example 16; Fig 43; 27pp; English.
 XX
 CC The invention relates to isolated nucleic acid sequences encoding
 CC elongase proteins and the elongase proteins themselves. Also
 CC included are a purified polypeptide which elongates polyunsaturated
 CC fatty acids and has at least 30% amino acid similarity to the amino acid
 CC sequence to an elongase protein, a vector comprising the nucleic
 CC acid, a plant cell (or tissue or whole plant) comprising the vector and
 CC expressing the nucleic acid, a plant oil or acid expressed by the
 CC transgenic plant and a transgenic non-human animal expressing elongase
 CC in its fluid. The nucleic acids and elongase proteins may be used
 CC directly or indirectly in the production of polyunsaturated fatty acids
 CC (puta); for a g arachidonic acid, which can then be used nutritional
 CC compositions, pharmaceutical compositions, cosmetics and animal feeds.
 CC The pharmaceutical compositions may be used in the treatment of
 CC restenosis after angioplasty, AIDS (acquired immunodeficiency syndrome),
 CC multiple sclerosis, inflammatory skin diseases, osteoporosis, kidney or
 CC urinary tract stones, malignant cancer, cachexia associated with cancer,
 CC eczema, symptoms of inflammation, rheumatoid arthritis, asthma and
 CC psoriasis. They are also useful for inhibiting platelet aggregation,
 CC inducing vasodilation, reducing cholesterol, reducing or preventing
 CC gastrointestinal bleeding and side effects of non-steroidal
 CC anti-inflammatory drugs. The present sequence encodes an elongase
 CC of the invention.
 XX
 SQ Sequence 914 BF; 236 A, 223 C, 199 G, 256 T, 0 other.

Alignment Scores:
 Pred. No.: 8,61e-161 Length: 914
 Score: 1558.00 Matches: 278
 Percent Similarity: 97.32% Conservative: 13
 Best Local Similarity: 92.98% Mismatches: 8
 Query Match: 94.37% Indels: 0
 DB: 24 Gaps: 0

US-09-624-670-64 (1-299) x ABK46367 (1-914)

Breast cancer; diagnosis; prognosis; detection; screening;
 antibody; oestrogen receptor; anti-oestrogen; immune response;
 lymph node; metastases; tumour; BCR3; BCQ8; BCQ5; BCR1; BCN2;

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 1 ATCGAACATTTTCATGCATCACTAGTACCTATTTCAGGCACTTCTAGGCTCTGAGAT 60
 21 ThrArgValLysGlyTyrPheLeuLeuAspAsnTyrIleProThrPheValCysSerVal 40
 61 ACTAGAGTAAGAGTGGTTCTCTGGCAATATATACCCACATTTATCTGTCTCTC 120
 41 IleTyrLeuLeuIleValTrpLeuGlyProLysTyrMetLysAsnArgGlnProPheSer 60
 121 ATATATTACTAATTGTATGGCTGGGACCAAAATACATGAGCAATAAACAGCAATCTCT 180
 61 CysArgGlyIleLeuGlnLeuTyrAsnLeuGlyLeuThrLeuLeuSerLeuTyrMetPhe 80
 181 TGCCTGGGGGATTTTACTGGTGTATTAACCTTGGACTCACACTGCTGTCTGTATATGTT 240
 81 TyrGluLeuValThrGlyValValTTPGluGlyLysTyrAsnPhePheCysGlnGlyThrArg 100
 241 TGTGAGTATGTAACAGGAGTATGGAAGGCAATACAACTTCTCTGTCAGGACACGC 300
 101 SerAlaGlyGluSerAspMetLysIleIleArgValLeuTyrTrpTyrPheSerLys 120
 301 ACCGACGAGATCAGATATGAAGATATCCGTTGCTCTCTGGTGTACTCTTCTCCAAA 360
 121 LeuIleGluPheMetAspThrPhePheIleLeuArgLysAsnAsnHisGlnIleThr 140
 361 CTCATAGAAATTTATGGACACTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 420
 141 ValLeuHisValTyrHisHisAlaThrMetLeuAsnIleThrPheValMetAsnTrp 160
 421 GTCTGTGACGCTACACCATGCTCGATGCTGAACATCTGGTGGTGTGTGTGTAAGTGG 480
 161 ValProCysGlyHisSerTyrPheGlyAlaThrLeuAsnSerPheIleHisValLeuMet 180
 481 GTCCCTCTGGGCTCCACTCTTATTTTGTGTGACACTTAATAGCTTCATCCACGTCCTATG 540
 181 TyrSerTyrTyrGlyLeuSerSerIleProSerMetArgProTyrLeuTrpLysLys 200
 541 TACTCTTACTATGCTTTTGTCTGCTCAGTCCCTTCCATCGCTCATACCTCTGCTGGAAGAAG 600
 201 TyrIleThrGlnGlyGlnLeuValGlnPheValLeuThrIleIleGlnThrCysGly 220
 601 TACATCA-TCAAGGATTA-TCTTTAGTTTGTGACAAATCATCCAGACACGACGCGGG 660
 221 ValPheTrpProCysSerPheProLeuGlyTyrPhePheGlnIleGlyTyrMetIle 240
 661 GTCATCTGGGCTGTCACATTTCCCTCTTGGTGTGTGTATTTCCAGATTGGATACATATT 720
 241 SerLeuIleAlaLeuPheThrAsnPheTyrIleGlnThrTyrAsnLysLysGlyAlaSer 260
 721 TCCCTGATGTCTCTCTTCCACAACTTCTACATTCAGACCTACAAAGAAAGGGGCTTC 780
 261 ArgArgLysAspHisLeuLysGlyHisGlnAsnGlySerValAlaAlaValAsnGlyHis 280
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 281 ThrAsnSerPheProSerLeuGluAsnSerValLysProArgLysGlnArgLysAsp 299
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 AC AAA54132;
 XX
 DT 08-FEB-2001 (first entry)
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 DE Breast cancer protein BCR2 coding sequence.
 XX
 KW Breast cancer; diagnosis; prognosis; detection; screening;
 KW antibody; oestrogen receptor; anti-oestrogen; immune response;
 KW lymph node; metastases; tumour; BCR3; BCQ8; BCQ5; BCR1; BCN2;

PA (UYJO) JOHN HOPKINS UNIVERSITY.
 XX Ishizaka K, Martens CL, Moore KW;
 DR WPI; 1988-280165/40.
 XX P-PSDB; AAP82590.
 XX Nucleic acid encoding glycosylation inhibiting peptide - capable of
 PT suppressing IgE immunoglobulin responses, for use as antiinflammatory
 PT agents.
 XX Claim 1; Page 16-21, 29pp, English.
 PS The sequence encodes a polypeptide with G1F activity, which has the
 XX following biological activities: IgE binding factor switching activity,
 CC inhibition of IgE-induced Fc epsilon receptor expression, and inhibition
 CC of phospholipase A2 activity after dephosphorylation.
 XX Sequence 2571 BP; 681 A; 573 C; 540 G; 777 T; 0 other;
 SQ

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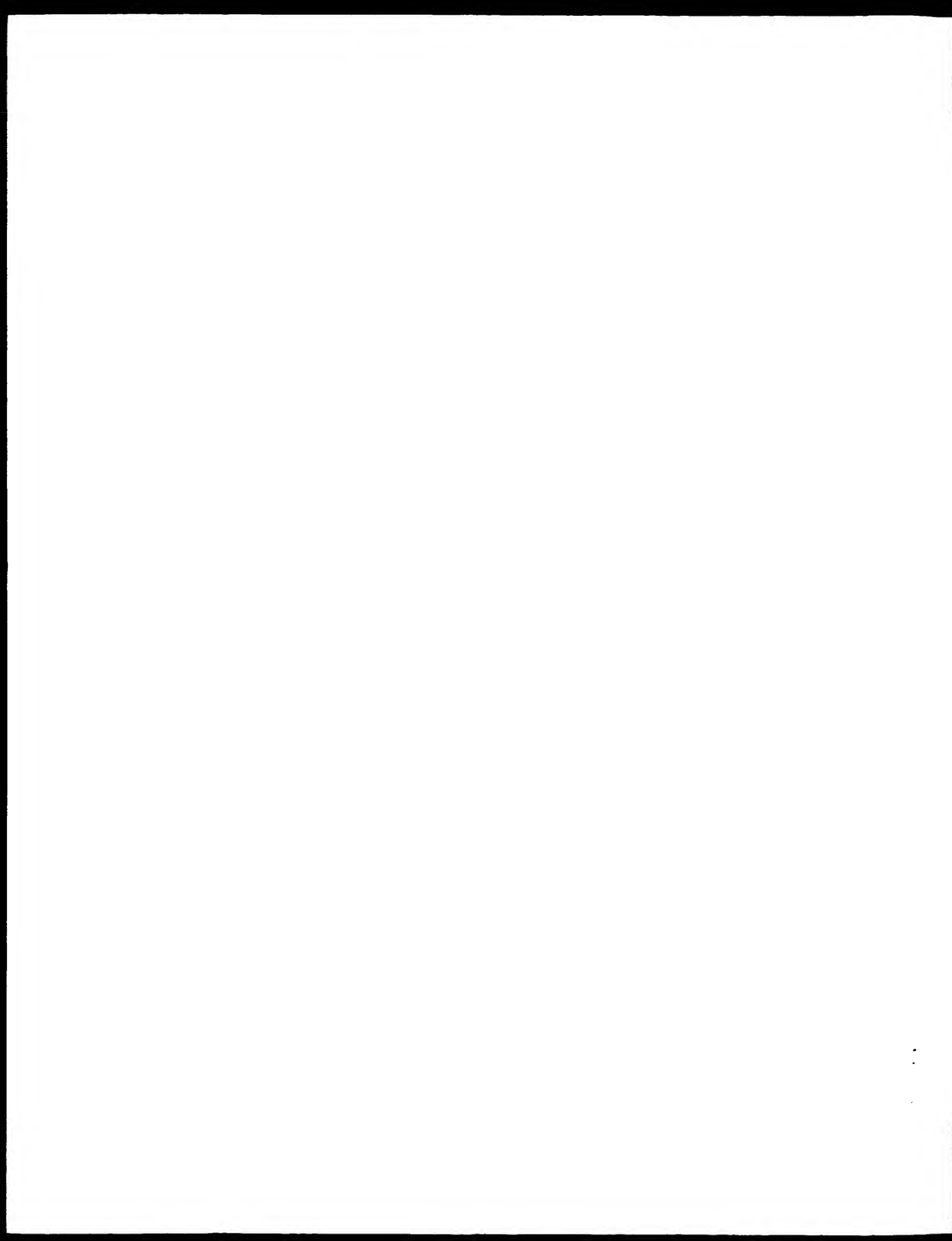
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 QY 47 TrpLeuGlyProLysTyrMetLysAsnArgGlnProPheSerCysArgGlyIleLeuGln 65
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 QY 67 LeuTyrAsnLeuGlyIleThrLeuLeuSerLeuTyrMetPheTyrGluLeuValThrGly 86
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 QY 87 ValTrpGluGlyLysTyrAsnPhePheCysGlnGlyThrArgSerAlaGlyGluSerAsp 106
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 QY 127 ThrPhePhePheIleLeuArgLysAsnAsnHisGlnIleThrValLeuHisValTyrHis 146
 Db 361 ATCTTTTCTTATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 420
 QY 147 HisAlaThrMetLeuAsnIleTyrTrpPheValMetAsuTrpValProCysGlyHisSer 156
 Db 421 CACCGTACCATCTCTCAACATC.....GTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 459
 QY 167 TyrPheGlyAlaThrLeuAsnSerPheIleHisValLeuMetTyrSerTyrTyrGlyLeu 186
 Db 460 TATTTCTGAGAAATATAAAGATATATATATATATATATATATATATATATATATAT 519
 QY 187 SerSerIleProSerMetArgTrpTyrLeuTrpTrpLysTyrIleThrGlnGlyGln 206
 Db 520 TCTCTATCTCTATCT 579
 QY 207 LeuValGlnPheValLeuThrIleIleGlnThrThrCysGlyValPheTrpProCysSer 226
 Db 580 CTGGGCTGAGT 639

QY 227 PheProLeuGlyTyrTrpLeuPhePheCInIleGlyTyrMetIleSerLeuIleAlaLeuPhe 246
 Db 640 TTCCTCTCGGAGTGGTCTTTCAGAGATTGGATACATGA-TTCCCTGATGTCTCTCTTC 699
 QY 247 ThrAsnPheTyrIleGlnThrTyrAsnLysLysGlyAlaSerArgArgLysAspHisLeu 266
 Db 700 ACAAACTTCTTACATTACAGCTTACAAAGAAAGGGCCCTCTCGGAGGAAGAACACCTG 759
 QY 267 LysGlyHisGlnAsnGlySerValAlaAlaValAsnGlyHisThrAsnSerPheProSer 286
 Db 760 AAGAGCAACAAAGAGGGTCTGTGGTCAAGCGGACACACCAACACCTTCCCTCTCC 819

QY 287 LeuGluAsnSerValLysProArgLysGlnArgLysAsp 299
 Db R20 CTGTAAGAAAGATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 358

RESULT 14
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 AC ABL90374;
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 DT 24-MAY-2002 (first entry)
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 DE Human polynucleotide SEQ ID NO 936.
 KW Cytostatic; immunosuppressive; nontropic; neuroprotective; antiviral;
 KW antiallergic; hepatocytropic; antidiabetic; antinflammatory; antiulcer;
 KW vulnary; anticonvulsant; antibacterial; antifungal; antiparasitic;
 KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
 KW neurological disease; infection; human; secreted protein; gene; ss.
 OS Homo sapiens.
 PN WO200190304-A2.
 PD 29-NOV-2001.
 XX
 PF 18-MAY-2001; 2001WO-US16450
 XX
 PR 19-MAY-2000, 2000US-205515P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Birse CE, Rosen CA
 XX
 DR WPI; 2002-132018/16.
 DR P-PSDB; ABB89965.
 XX
 PT Novel 1405 isolated polypeptides, useful for diagnosis, treatment and
 PT prevention of neural, immune system, muscular, reproductive,
 PT gastrointestinal, pulmonary, cardiovascular, renal and proliferative
 PT disorders -
 PS
 PS Claim 4; SEQ ID NO 936; 2081pp + Sequence listing; English.
 CC The invention relates to novel genes (ABL9449-ABL90853) and proteins
 CC (AAB89440-AAB99444) useful for preventing, treating or ameliorating
 CC medical conditions e.g. by protein or gene therapy. The genes are
 CC isolated from a range of human tissues disclosed in the specification.
 CC The nucleic acids, proteins, antibodies and (auto)agonists are useful
 CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
 CC and ovarian cancer and other cancers of the adrenal gland, bone, bone
 CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital,
 CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune
 CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
 CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative
 CC colitis; (c) cardiovascular disorders such as myocardial ischaemia;
 CC (d) wound healing; (e) neurological diseases e.g. cerebral ischaemia;
 CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
 CC and parasitic infections.
 CC Note: The sequence data for this patent did not form part of the



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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 15, 2003, 21:38:16 ; Search time 54.6396 Seconds
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1678.203 Million cell updates/sec

US-09-624-670-64

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Total number of hits satisfying chosen parameters:	882724
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Post-processing: Minimum Match 0%

Maximum Match	Maximum Match	Maximum Match
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Listing first 45 summaries

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Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2	476.5	28.9		1542	4	US-09-149-476-106	Sequence 106, App
3	3	326.5	19.8		1854	1	US-08-249-420-1	Sequence 1, Appl
4	4	326.5	19.8		1854	2	US-08-737-663-1	Sequence 1, Appl
5	5	255	15.4		590	4	US-09-145-828A-10	Sequence 10, Appl
6	6	249	15.1		954	4	US-09-145-828A-1	Sequence 1, Appl
7	7	219	13.3		989	1	US-07-885-970A-7	Sequence 7, Appl
8	8	219	13.3		989	1	US-08-298-687A-7	Sequence 7, Appl
9	9	219	13.3		989	1	US-08-530-797-6	Sequence 6, Appl
10	10	219	13.3		989	1	US-08-298-629-7	Sequence 7, Appl
11	11	219	13.3		989	2	US-08-787-335-6	Sequence 6, Appl
12	12	209	12.7		587	4	US-09-145-828A-9	Sequence 9, Appl

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Db 253 AAGCCCTCCAGCTCCGTCGCTTCATGATTCGTACAACTTCTCACIGGTCGACTCTCC 312
QY 77 LeuTyrMetPheTyrGluLeuValThrGlyValTrpGluGlyLysTyrAsnPhePheCys 96
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QY 228 ProLeuGlyTrpLeuPhePheGlnIleGlyTyrMetIleSerLeuIleAlaLeuPheThr 247
Db 793 CACCTCATCTGGATGATGTCGACCATCTTCTTCATG-----CTGTTCTCC 837
QY 248 AsnPheTyrIleGlnThrTyrAsnLysLysGlyAlaSerArgLysAspHisLeuLys 267
Db 838 AACTCTGTTATCACTCTTATACCAAG-----GGCAAGCGGCTGCCCCGTGTCATTCAG 891
QY 268 GlyHisGlnAsnGlySer-----ValAlaAlaValAsnGlyHisThrAsnSerPhePro 285
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RESULT 2
US-09-149-476-106
Sequence 106, Application US/09149476
Patent No: 64,0526
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: P2002P1
CURRENT APPLICATION NUMBER: US/09/149,476
CURRENT FILING DATE: 1998-09-08
EARLIER APPLICATION NUMBER: PCT/US98/04493
EARLIER FILING DATE: 1998-03-06
EARLIER APPLICATION NUMBER: 60/040,162
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EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,598
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,613

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 7 EARLIER FILING DATE: 1997-05-23
 8 EARLIER APPLICATION NUMBER: 60/047,632
 9 EARLIER FILING DATE: 1997-05-23
 10 EARLIER APPLICATION NUMBER: 60/047,601
 11 EARLIER FILING DATE: 1997-05-23
 12 EARLIER APPLICATION NUMBER: 60/043,580
 13 EARLIER FILING DATE: 1997-04-11
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 35 EARLIER APPLICATION NUMBER: 60/043,576
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 56 EARLIER FILING DATE: 1997-08-22
 57 EARLIER APPLICATION NUMBER: 60/056,908
 58 EARLIER FILING DATE: 1997-08-22
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 60 EARLIER FILING DATE: 1997-06-06
 61 EARLIER APPLICATION NUMBER: 60/057,650
 62 EARLIER FILING DATE: 1997-09-05
 63 EARLIER APPLICATION NUMBER: 60/056,884
 64 EARLIER FILING DATE: 1997-08-22
 65 EARLIER APPLICATION NUMBER: 60/057,669
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 67 EARLIER APPLICATION NUMBER: 60/049,610
 68 EARLIER FILING DATE: 1997-06-14
 69 EARLIER APPLICATION NUMBER: 60/061,060
 70 EARLIER FILING DATE: 1997-10-02

Alignment Scores:

Pred. No.:

3,450,48

Length:

1942

TITLE OF INVENTION: GENETICALLY ENGINEERING COTTON
 TITLE OF INVENTION: PLANTS FOR ALTERED FIBER

NUMBER OF SEQUENCES: 33
 CORRESPONDENCE ADDRESS:

APPLICANT: Nicholas J. Seay, Quaries & Brady
 ADDRESS: P.O. Box 2113, First Wisconsin Plaza

CITY: Madison
 STATE: Wisconsin

COUNTRY: USA
 ZIP: 53701

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Microsoft Word
 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/298,687A
 FILING DATE:

CLASSIFICATION: 800
 PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/617,239
 FILING DATE: 21-NOV-1990

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/253,243

FILING DATE: 04-OCT-1988
 ATTORNEY/AGENT INFORMATION:

NAME: Seay, Nicholas J.
 REGISTRATION NUMBER: 27,386

TELEPHONE: (608) 283-2478
 TELEFAX: (608) 261-5139

INFORMATION FOR SEQ ID NO. 7:
 SEQUENCE CHARACTERISTICS:

LENGTH: 989 base pairs
 TYPE: nucleic acid

STRANDEDNESS: double
 TOPOLOGY: linear

MOLECULE TYPE: cDNA
 HYPOTHETICAL: NO

ANTI-SENSE: NO
 ORIGINAL SOURCE:

ORGANISM: Gossypium hirsutum
 STRAIN: Coker 312

DEVELOPMENTAL STAGE: 10 day old fiber cells
 TISSUE TYPE: fiber cells

IMMEDIATE SOURCE:
 LIBRARY: CREFB10

CLONE: All
 US-08-298-687A-7

Alignment Scores:
 Prod. No. Length 989

Score: 219.00 Matches: 56

Percent Similarity: 63.8% Conservatives: 35

Best Local Similarity: 43.14% Mismatches: 58

Query Match: 13.2% Indels: 20

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US-09-624-670-64 (1-299) x US-08-298-687A-7 (1-989)

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DB 937 TTCCCTAGGGACATCCCAACGGGCTT-----CCTCTTTC 899

QY 115 Trp-----TyrTyrPheSerLysLeuIleGluPheMetAspThrPhePheIle 131

DB 898 TGGGATAATATTTTACTTTTAAATTCTTCAATATGSAACCTTTTCAATAT 849

QY 132 IcuArgLysAsnAsnHisGlnIleThrValLeuHisValTyrHisHisAlaThrMetIeu 151

DB 838 CTCACGGGAICACAAAGAGTAATCTTCTTACGCTACTCACTCATCATGCGTC 779

QY 152 AsnIleTrpTrpPheValMetAsnTrpValProCysGlyHisSerTyrPheGlyAlaThr 171

DB 778 ATCATGCTTATATTTCATTAGACATGCTCAGTCTCCTGTAACCATGGTGTGATCACC 719

QY 172 LeuAsnSerPheIleHisValIleuMetTyrSerTyrTyrGlyLeuSerSerIleProSer 191

DB 718 ---AACTGCTGTATGCAATGTAATACTGACTCTGTAATACCTGTGTGACACCTG---GGG 665

QY 192 MetArgProTyrLeuTrpTrpLysLysTyrIleThrGlnGlyGlnLeuValGlnPheVal 211

DB 884 AIGTACCTTAA3-----TGGACAGAAAGAGTGAAGGATTTTAACTGAGTGTGCTTCGG 611

QY 212 LeuThrIleLeuGlnThrThrCysGlyValPheTrp-----ProCysSer 226

DB 516 TTAAGTTTCTTATCATGAGGATGTTGTTGTTTATGTTTATGTTTATGTTTATGTTT 551

QY 227 PheTyrGlyGlyTyrPhePhePheGlnIleGlyTyrMetIleSerLeuIleAlaIlePhe 246

DB 550 GGGATTCTGAGTGTGTST---TTCAATGAGAGCTTCAAGCTCTCTTCTTCTTCTTCTT 494

QY 247 ThrAsnPheTyrIleGlnThrThrAsn 255

DB 493 TCAGACTTTTCATGCCAGAGTTACTCC 467

RESULT 9
 US-08-530-797-6/c

: Sequence 6, Application US/08530797
 : Patent No. 5597718

: GENERAL INFORMATION:
 : APPLICANT: John, Maliyakal E.

: APPLICANT: Umbeck, Paul F.
 : APPLICANT: Brill, Winston J.

: TITLE OF INVENTION: GENETICALLY ENGINEERED COTTON PLANTS
 : NUMBER OF SEQUENCES: 18

: CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Quaries and Brady

: STREET: P.O. Box 2113
 : STREET: FIRST WISCONSIN PLAZA

: CITY: MADISON
 : STATE: WISCONSIN

: COUNTRY: U.S.A.
 : ZIP: 53701

: COMPUTER READABLE FORM:
 : MEDIUM TYPE: Diskette - 3.50 inch, 800kb storage

: COMPUTER: Apple Macintosh
 : OPERATING SYSTEM: Macintosh

: SOFTWARE: Microsoft Word 4.0
 : CURRENT APPLICATION DATA:

: APPLICATION NUMBER: US/08/530,797
 : FILING DATE: 20-SEP-1995

: CLASSIFICATION: 800
 : PRIOR APPLICATION DATA:

: APPLICATION NUMBER: 07/617,239
 : FILING DATE: 21-NOV-90

: APPLICATION NUMBER: US 07/253,243
 : FILING DATE: 04-OCT-88

: ATTORNEY/AGENT INFORMATION:
 : NAME: Nicholas J. Seay

: REGISTRATION NUMBER: 27,386
 : REFERENCE/DOCKET NUMBER: 1122990245

: INFORMATION FOR SEQ ID NO. 6:
 : SEQUENCE CHARACTERISTICS:

: LENGTH: 989 base pairs
 : TYPE: nucleic acid

: STRANDEDNESS: single
 : TOPOLOGY: linear

: MOLECULE TYPE: cDNA to mRNA
 : HYPOTHETICAL: no

: ANTI-SENSE: no
 : ORIGINAL SOURCE:

: ORGANISM: Gossypium hirsutum
 : STRAIN: Coker 312

: DEVELOPMENTAL STAGE: 10 day old fiber cells


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DB 610 TTAAGCTTTTGAACAGAGGACAGCTTGGTGTCTACCACTTCACCTTCCTCGGCTGCTCT 551
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RESULT 11
US-08-787-335-6/c
: Sequence 6, Application US/08787335
: Patent No. 5981834
: GENERAL INFORMATION:
: APPLICANT: John, Maliyakal E.
: APPLICANT: Umbeck, Paul F.
: APPLICANT: Brill, Winston J.
: TITLE OF INVENTION: GENETICALLY ENGINEERED COTTON PLANTS
: NUMBER OF SEQUENCES: 18
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Quarles and Brady
: STREET: P.O. BOX 2113
: STREET: FIRST WISCONSIN PLAZA
: CITY: MADISON
: STATE: WISCONSIN
: COUNTRY: U.S.A.
: ZIP: 53701
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette - 3.50 inch, 800kb storage
: COMPUTER: Apple Macintosh
: OPERATING SYSTEM: Macintosh
: SOFTWARE: Microsoft Word 4.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/787,335
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/530,797
: FILING DATE:
: APPLICATION NUMBER: 04-OCT-88
: ATTORNEY/AGENT INFORMATION:
: NAME: Nicholas J. Seay
: REGISTRATION NUMBER: 27,386
: REFERENCE/DOCKET NUMBER: 1122990245
: INFORMATION FOR SEQ ID NO: 6:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 989 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA to mRNA
: HYPOTHETICAL: no
: ANTI-SENSE: no
: ORIGINAL SOURCE:
: ORGANISM: Gossypium hirsutum
: STRAIN: Coker 312
: DEVELOPMENTAL STAGE: 10 day old fiber cells
: TISSUE TYPE: fiber cells
: IMMEDIATE SOURCE:
: LIBRARY: CKFB10
: CLONE: All
US-08-787-335-6

Alignment Scores:
Pred. No.: 3 88e-17 Length: 989
Score: 219.90 Matches: 56
Percent Similarity: 53.8% Conservative: 35
Best Local Similarity: 53.14% Indels: 58
Query Match: 13.26% Indels: 20

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QY 115 TTP-----TyrTyrPheSerLysLeuIleGluPheMetAspThrPhePhePheIle 131
DB 898 TGGGCATACATCTCTACCTCCCAAGATTGTGAATTCATGGACACCCCTTTGATCATC 839
QY 132 LeuATGlyAsnAsnHisGlnIleThrValLeuHisValTyrHisHisAlaThrMetLeu 151
DB 838 CTCAGCGGATCATGAGAGGTATCTCTCTTCCCTACGCTACCATCATCGTGGTGC 779
QY 152 AsnIleTrpTrpPheValMetAsnTrpValProCysGlyHisSerTyrPheGlyAlaThr 171
DB 778 ATCATGTGTATATTGCTTAGACAGCTGCTCAGTCTCCGACCATGGTCTGATCACC 719
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RESULT 12
US-09-145-828A-5
: Sequence 9, Application US/09145828A
: Patent No. 6403349
: GENERAL INFORMATION:
: APPLICANT: Abbott Laboratories
: APPLICANT: Mukerji, Pradip
: APPLICANT: Leonard, Amanda E. Y.
: APPLICANT: Fuang, Yung-Sheng
: APPLICANT: Thurmond, Jennifer
: APPLICANT: Kirchner, Stephen J.
: APPLICANT: Farber-Barnes, Jennifer M.
: TITLE OF INVENTION: THE ELONGASE GENE AND USES THEREOF
: FILE REFERENCE: 6407-US-01
: CURRENT APPLICATION NUMBER: US/09/145,828A
: CURRENT FILING DATE: 1998-09-02
: NUMBER OF SEQ ID NOS: 30
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO: 9
: LENGTH: 587
: TYPE: DNA
: ORGANISM: Mortierella alpina
US-09-145-828A-9

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Score: 209.00 Matches: 58
Percent Similarity: 49.50% Conservative: 42
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US-09-624-670-64 (1-299) x US-09-145-828A-9 (1-587)

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[illegible]

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd

OM protein - nucleic search, using frame_plus_f2n model

Run on: June 15, 2003, 23:02:06 ; Search time 131.034 seconds
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3304.262 Million cell updates/sec

Title: US-09-624-670-64

Perfect score: 1651

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Database :

Published Applications_NA:*

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13: /cgn2_6/ptodata/1/pubpna/us06_NEW_PUB seq.*
14: /cgn2_6/ptodata/1/pubpna/us06_PUBCOMB seq.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1651	100.0	900	10	us-09-903-456-6 Sequence 6, Appli
2	1558	94.4	914	10	us-09-903-456-3 Sequence 3, Appli
3	1108	67.1	871	9	us-09-764-888-453 Sequence 353, App
4	1089	64.7	748	9	us-09-764-888-352 Sequence 452, App

5	956.5	57.9	879	9	us-09-849-199A-22 Sequence 22, Appli
6	956.5	57.9	879	10	us-09-903-456-5 Sequence 5, Appli
7	954.5	57.8	2426	9	us-10-138-846-13406 Sequence 13406, A
8	724	43.9	2225	10	us-09-925-301-248 Sequence 248, App
9	548	33.2	384	9	us-09-918-995-37438 Sequence 37438, App
10	452	28.8	430	9	us-09-918-995-17480 Sequence 17480, A
11	476.5	28.9	1482	9	us-09-809-391-258 Sequence 258, App
12	476.5	28.9	1542	9	us-09-809-391-106 Sequence 106, App
13	445	27.0	1682	10	us-09-822-830A-345 Sequence 345, App
14	395.5	24.0	819	10	us-09-903-456-7 Sequence 7, Appli
15	395.5	24.0	819	10	us-09-903-456-72 Sequence 72, Appli
16	391.5	23.7	819	10	us-09-903-456-73 Sequence 73, Appli
17	390.5	23.7	819	10	us-09-903-456-70 Sequence 70, Appli
18	388.5	23.5	818	10	us-09-903-456-71 Sequence 71, Appli
19	386.5	23.4	819	10	us-09-903-456-69 Sequence 69, Appli
20	385.5	23.3	819	10	us-09-903-456-74 Sequence 74, Appli
21	381.5	23.1	957	10	us-09-903-456-2 Sequence 2, Appli
22	358	21.7	549	9	us-09-931-936-1727 Sequence 1727, Ap
23	332	20.1	196	10	us-09-864-761-19026 Sequence 19026, A
24	332	20.1	212	10	us-09-864-761-26863 Sequence 26863, A
25	332	20.1	409	10	us-09-864-761-33069 Sequence 33069, A
26	332	20.1	485	10	us-09-864-761-2289 Sequence 2289, Ap
27	332	20.1	8861	9	us-09-764-868-1445 Sequence 1445, Ap
28	328	19.9	455	10	us-09-864-761-10225 Sequence 10225, A
29	294	17.8	630	10	us-09-903-456-67 Sequence 67, Appli
30	276.5	16.7	447	9	us-09-918-995-9957 Sequence 9957, Ap
31	260	15.7	24664	9	us-10-073-961-613 Sequence 613, App
32	260	15.7	24664	10	us-09-764-887-613 Sequence 613, App
33	255	15.4	590	10	us-09-903-456-17 Sequence 17, Appli
34	249	15.1	954	10	us-09-903-456-1 Sequence 1, Appli
35	246.5	14.9	867	10	us-09-903-456-4 Sequence 4, Appli
36	232	14.1	1387	9	us-10-138-846-12745 Sequence 12745, A
37	227	13.7	2775	9	us-10-161-521A-3 Sequence 3, Appli
38	227	13.7	2989	9	us-09-759-130B-221 Sequence 221, App
39	217	13.1	795	9	us-09-759-130B-222 Sequence 222, App
40	217	13.1	798	10	us-09-903-456-63 Sequence 63, Appli
41	216	13.1	813	9	us-09-759-130B-238 Sequence 238, App
42	209	12.7	587	10	us-09-903-456-16 Sequence 16, Appli
43	209	12.1	167	10	us-09-783-590-46 Sequence 46, Appli
44	189	10.1	511	9	us-09-918-995-43797 Sequence 43797, A
45	164	9.9	470	9	us-09-918-995-968 Sequence 968, App

ALIGNMENTS

RESULT 1
US-09-903-456-6
Sequence 6, Application US/09093456
Patient No. US20020138874A1
GENERAL INFORMATION:
APPLICANT: Mukerji, Pradip
APPLICANT: Leonard, Amanda Eun-Yeong
APPLICANT: Huang, Yung-Sheng
APPLICANT: Pereira, Suzette L.
TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF
FILE REFERENCE: 6407.US.P3
CURRENT FILING DATE: 2001-07-11
CURRENT FILING NUMBER: US/09/903.456
PRIOR APPLICATION NUMBER: US 09/624,670
PRIOR FILING DATE: 2000-07-24
PRIOR APPLICATION NUMBER: US 09/379,095
PRIOR FILING DATE: 1999-08-23
PRIOR APPLICATION NUMBER: US 09/145,828
PRIOR FILING DATE: 1998-09-02
NUMBER OF SEQ ID NOS: 116
SOFTWARE: FASTSQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 900
TYPE: DNA
ORGANISM: Mus musculus
US-09-903-456-6

Alignment Scores:

Pred. No.: 1,2e-101 Length: 879
 Score: 956.50 Matches: 168
 Percent Similarity: 71.58% Conservatively: 36
 Best Local Similarity: 58.95% Mismatches: 78
 Query Match: 57.93% Indels: 3
 DB: 10 Gaps: 1

US-09-624-670-64 (1-299) x US-09-903-456-5 (1-879)

```

QY 1 MetGluHisPheAspAlaSerLeuSerThrTyrPheLysAlaPheLeuGlyProAsp 20
DB 10 CTGAAGGCTTGTGATTAATGAAATGTTTATGGAACAAAGTTTGAACAGAGAT 54
QY 2 ThrAlaValLysGlyTrpPheLeuLeuAspSerVal 40
DB 70 TCTGAGTTCGGGGTGGTTCGCTGGACTTACCTCCACCTTCACTCCACCATC 129
QY 41 IleTyrLeuLeuValTrpLeuGlyProLysTyrMetLysAsnArgGlnProPheSer 60
DB 130 AGCTACCTCTCTCCGATATAGGCTGGGTAACAGATACAGAAAGACAGGCTCTCTGCT 189
QY 61 CysArgGlyLysGlnLeuTyrAsnLeuGlyLeuThrLeuSerLeuTyrMetPhe 80
DB 190 ATGAGGATGCTATATGATTAAGCTCCGAAACACTTCTTTTACGATATATGCTG 249
QY 81 TyrGluLeuValThrGlyValTrpGlyLysTyrAsnPheCysGlnGlyThrArg 100
DB 250 GTGGAGCTCATCTCTCCAGCTGGGAGGAGGTATACAACTTGCAGTCTCAAACTCCGAC 309
QY 101 SerAlaGlyLysSerAspMetLysIleIleArgValLeuTrpTyrPheSerLys 120
DB 310 AGTGAGGAGAGAGTGAAGTGGGTGAGTCAAGGTCCTGGGAGGTAACACTCTCCAAA 369
QY 121 LeuIleGluPheMetAspThrPhePheIleLeuArgLysAsnAsnHisGlnIleThr 140
DB 370 CTATGGAGTTCCTGGACAGATTTCTTCTTCTAGCAAAAAGACAAATCAGATCAC 429
QY 141 ValLeuHisValTyrHisAlaThrMetLeuAsnIleTrpTrpPheValMetAsnTrp 160
DB 430 TTCCCTTCATGCTATACACCGGCGCATGTTCAACATCTGGTGTGTGTGAACTGG 489
QY 161 ValProCysGlyHisSerTyrPheGlyAlaThrLeuAsnSerPheIleHisValLeuMet 180
DB 490 ATACCTTGTGTCACAAAGCTCTTGGACCCACCTGAACAGCTTATCCACATCTCATC 549
QY 181 TyrSerTyrTyrGlyLeuSerSerIleProSerMetArgProTyrLeuTyrTyrLys 200
DB 550 TACTCTACTACATATATTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 609
QY 201 TyrIleThrGlnGlyGlnValGlnPheValIleThrIleIleGlnThrThrCysGly 220
DB 610 IACCTACACACACACACACACACACACACACACACACACACACACACACACACAC 659
QY 221 ValPheTrpProCysSerPheProLeuGlyTrpLeuPheGluTyrMetIle 240
DB 670 GTGGTCAACCTCTGTGGCTTCCCTTGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 729
QY 241 SerLeuIleAlaLeuPheThrAsnPheTyrIleGlnThrTyrAsnLysLysGlyAlaSer 260
DB 730 ACATGATATATATATATATATATATATATATATATATATATATATATATATATAT 789
QY 261 Arg-----ArgLysAspHisLysGlyHisGlnAsnGlySerValAlaAlaVal 277
DB 790 AAACACCTCCACAGACAGAAAGATTAATATGTTTCTCCCAAAAGCCCACTTAATTTGGGCT 849
QY 278 AsnGlyHisThrAsn 282
DB 850 AATGGCATGACGGAC 864

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RESULT 7

US-10-198-846-13406

: Sequence 1406, Application US/1019846

```

: Publication No. US20030094974A1
: GENERAL INFORMATION:
: APPLICANT: Billie, James
: APPLICANT: Xu, Yongyao
: APPLICANT: Wang, Youzhen
: APPLICANT: Steinmann, Kathleen
: TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
: TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
: FILE REFERENCE: MRI-049
: CURRENT APPLICATION NUMBER: US/10/198,846
: PRIOR FILING DATE: 2003-07-18
: PRIOR APPLICATION NUMBER: 60/306,220
: PRIOR FILING DATE: 2001-07-18
: NUMBER OF SEQ ID NOS: 14084
: SOFTWARE: FastSeq For Windows Version 4.0
: SEQ ID NO 13436
: LENGTH: 2425
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc.feature
: LOCATION: 1, 2425, 2425
: OTHER INFORMATION: n = A,T,C or G
: US-10-198-846-13406

```

Alignment Scores:

Pred. No.: 9,79e-101 Length: 2426
 Score: 954.50 Matches: 173
 Percent Similarity: 70.47% Conservatively: 37
 Best Local Similarity: 58.05% Mismatches: 81
 Query Match: 57.81% Indels: 7
 DB: 9 Gaps: 3

US-09-624-670-64 (1-299) x US-10-198-846-13406 (1-2426)

```

QY 1 MetGluHis-----PheAspAlaSerLeuSerThrTyrPheLysAlaPheLeuGly 17
DB 85 ATGGAAACATCTAAAGCCCTTTCATCATCAAAATCAATCGCTTTTGGACAATATGTTGGA 144
QY 18 ProArgAspThrArgValLysGlyTrpPheLeuLeuAspAsnTyrIleProThrPheVal 37
DB 145 CTGCGAGATTCCTCGAGTCAGAGGTGGTTCATGTTGGACTTACCTTCCTACCTTTT 204
QY 38 CysSerValIleTyrLeuLeuValTrpLeuGlyProLysTyrMetLysAsnArgGln 57
DB 205 CTTACTGTTCATGATATCTCTCTCAAAATGGGCTGGTAAAGATATATGAAGACAGACCT 264
QY 58 ProPheSerCysArgGlyIleLeuGlnLeuTyrAsnLeuGlyLeuThrLeuLeuSerLeu 77
DB 265 GCTCTTCTCTCAGGGGTATCTCACCCTGTATATATCTTGAATACACACTTCTCTCGCG 324
QY 78 TyrMetPheTyrGluLeuValThrGlyValTrpGluGlyLysTyrAsnPheCysGln 97
DB 325 TACATGTTGAGAAAGTCACTCTCTCTCAATTTGGTAAAGAGCTTCAAACTTACAGTGC 384
QY 98 GlyThrArgSerAlaGlyGluSerAspMetLysIleIleArgValLeuTrpTrpTyr 117
DB 385 CATCTTACCGCGCAGCGGAAAGCTCACAATCGGCTAGCGAGTGTCTTGGTGTACTAT 444
QY 118 PheSerLysLeuIleGluPheMetAspThrPhePheIleLeuArgLysAsnAsnHis 137
DB 445 TTCTCCAAATCAGTAGAGTCTCTGACACAATTTCTCTGTTTGGCGAAAAAACAGAGT 504
QY 138 GlnIleThrValLeuHisValTyrHisHisAlaThrMetLeuAsnIleTrpTrpPheVal 157
DB 505 CAGATTACTTTTCTTCATGATATCATCATCTCTCTCTCTCTCTCTCTCTCTCTCTCT 564
QY 158 MetAsnTrpValProCysGlyHisSerTyrPheGlyAlaThrLeuAsnSerPheIleHis 177
DB 565 TTGAACCTGGAACCTTGTGGACAAAGTTCTTTGGACCAACACTGAACACTTTATCCAC 624
QY 178 ValLeuMetTyrSerTyrTyrGlyLeuSerSerIleProSerMetArgProTyrLeuTrp 197

```


[illegible]

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd

CM protein nucleic search, using frame_plus_p2n model

Run on June 15, 2003, 21:36:46: Search time: 1190.54 seconds
(without alignments)
4066 072 Million cell updates/sec

Title:

Perfect score

Sequence:

US-09-624-670-64

1 MHHFASISTYFKAFICPPQ HTNSFPS: FNSVPRKPKD 299

Scoring table:

BLOSUM62

Xgapop 10.0, Xgapext 0.5

Ygapop 10.0, Ygapext 0.5

Fgapop 6.0, Fgapext 7.0

Dgapop 6.0, Dgapext 7.0

Searched:

16154066 seqs, 809774376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing:

Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-G=us-09-624-670-64

-DB=FASTA

-OUTFMT=FASTA

-UNITS=bits

-LOCAL=200

-OUTFMT=FASTA

-NO_MMALP

-DEF_TIMEOUT=120

-FCGAPEXT=7

Database:

1: em_estba:*

2: em_esthum:*

3: em_estlin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_hic:*

9: gb_est1:*

10: gb_est2:*

11: gb_hic:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: gb_gss:*

18: em_gss_hum:*

19: em_gss_inv:*

20: em_gss_pla:*

21: em_gss_vrt:*

22: em_gss_fun:*

23: em_gss_hum:*

24: em_gss_mus:*

25: em_gss_of:*

26: em_gss_pro:*

27: em_gss_tod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1530	92.7	941	9	AL559414	AL559414 AL559414
2	1402	84.9	900	13	BI693107	BI693107 603344472
3	1351.5	81.9	950	9	AL553407	AL553407 AL553407
4	1337	80.4	897	14	H0884363	H0884363 AGENCOURT
5	1309	79.3	861	9	AL514872	AL514872 AL514872
6	1300	78.7	843	14	H0217076	H0217076 AGENCOURT
7	1290.5	78.2	991	14	H0895704	H0895704 AGENCOURT
8	1219	73.8	785	9	A0079897	A0079897 A0079897
9	1217.5	73.7	700	13	H1155440	H1155440 602903816
10	1178	71.4	902	9	AL516234	AL516234 AL516234
11	1164.5	70.5	932	9	AL552819	AL552819 AL552819
12	1164	70.5	961	14	H0936171	H0936171 AGENCOURT
13	1158	70.1	375	13	RI853179	RI853179 603379527
14	1152	59.8	397	14	H0213770	H0213770 AGENCOURT
15	1140	59.0	561	10	H080106	H080106 RC4-RT062
16	1132	58.0	796	10	H0535118	H0535118 601231235
17	1119	67.8	760	9	AL548756	AL548756 AL548756
18	1119	67.8	787	13	RI597218	RI597218 603250986
19	1113.5	67.4	884	13	RI758566	RI758566 603023086
20	1113	67.4	885	12	H0128078	H0128078 602353438
21	1112.5	67.4	862	13	RI835075	RI835075 603087730
22	1091	66.1	927	12	H0173950	H0173950 60234023
23	1053	63.8	748	12	H0270622	H0270622 188609.7
24	1047	63.4	712	13	BI327811	BI327811 602979561
25	1046	63.4	716	14	RI328570	RI328570 602985371
26	1042.5	63.1	712	14	H0371432	H0371432 602843085
27	1042	63.0	582	12	H0992305	H0992305 MK3-07009
28	1032.5	62.5	907	12	H0100925	H0100925 601753670
29	1032	62.5	810	12	H0251449	H0251449 602363905
30	997.5	60.4	800	13	BI568778	BI568778 603294725
31	995	60.3	735	9	AL518949	AL518949 AL518949
32	990	60.0	666	10	H0559205	H0559205 H0559205
33	987	59.8	694	14	RM788585	RM788585 K-EST0067
34	970	58.9	635	10	H0615265	H0615265 H0615265
35	956.5	57.9	800	11	AK014803	AK014803 Mus muscu
36	952	57.7	627	10	BB613066	BB613066 BB613066
37	927	56.1	1150	13	BM461375	BM461375 AGENCOURT
38	925.5	56.1	969	12	BF161512	BF161512 601771006
39	923	55.9	712	13	H0523961	H0523961 H0523961
40	897	54.3	694	12	H0721563	H0721563 602695171
41	887	53.7	620	10	BB657364	BB657364 BB657364
42	885	53.6	677	10	BB643510	BB643510 BB643510
43	881	53.4	614	10	BB661704	BB661704 BB661704
44	877.5	53.1	749	13	BI463309	BI463309 603204321
45	870	52.7	1028	14	H0895633	H0895633 AGENCOURT

ALIGNMENTS

RESULT 1
AL559414

LOCUS

DEFINITION

AL553414 L11_NFL008_T02 Homo sapiens cDNA clone CS0DJ013VD07 5

prime, mRNA sequence.

ACCESION

AL559414

VERSION

AL559414.1

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 941)

AUTHORS

Li, W.-H., Gruber, C., Li, S.-S., Li, J. and colleagues, et al.

TITLE

Full-length cDNA libraries and normalization

QY 161 ValProCysGlyHisSerIlePheGlyAlaThrLeuAsnSerIleHisValLeuMet 180
 DB 602 GTCCCTCGGGGACTTATTTGGTGGCCACATTAATATAGTTCATGACAGGCTCATG 561
 QY 181 TyrSerTyrTyrGlyLeuSerSerIleProSerMetAlaProTyrLeuTyrTrpLysLys 200
 DB 662 TACTCTTACTATGGTTTGTGTACCTCCCTCCATGCTGCATACCTCTGGTGGCAAG 721
 QY 201 TyrIleThrIleGlyLeuValGlyPheValLeuThrIleIleGlyThrThrCysGly 220
 DB 742 TATATCATCATGAGGCAATCTTATTTATTTATTTATTTATTTATTTATTTATTTAT 781
 QY 221 ValPheThrProCysSerPheProValGlyPheThrIleGlyThrIleGlyTyrMetIle 240
 DB 782 GTCACTGCTGCTGCAATTCCTCTGTTGGTGTGA TTTCAGATTGATATCATGATT 840
 QY 241 SerLeuIleAlaLeuPheThrAsnPheTyrIleLeuThrTyrAsnLysLysGlyAlaSer 260
 DB 841 TCCCTGATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 899
 QY 261 ArgArgLysAspHisIleGlyGlyHisAsnSerIle 273
 DB 900 CGAAGGAAGACACAT GAAGACACACAGAAATGGGTCA 936

RESULT 4
 BQ883263
 LOCUS
 DEFINITION AGNCOURT_8727526 NIH_MGC_47 Homo sapiens cDNA clone IMAGE:6340766
 5' UTR mRNA sequence.

ACCESSION BQ883263
 VERSION BQ883263.1 GI:22275271
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 897)
 AUTHORS NIH-MGC <http://mgi.nhlbi.nih.gov/>
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cdapubs@nhi.nih.gov
 Tissue procurement: ATCC
 cDNA library preparation: Rubin Laboratory
 cDNA library arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: tACM2537 row: 1 column: 15
 High quality sequence stop: 688.

FEATURES
 Location/Qualifiers
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 /db_xref="taxon:9606"
 /cclone="IMAGE:6340766"
 /clone_lib="NIH_MGC_47"
 /tissue_type="neuroblastoma, cell line"
 /lab_host="DH10B (phage resistant)"
 /note="organ: brain; Vector: pORI7; site_1: XhoI; site_2:
 EcoRI; cDNA made by oligo-dT priming. Directionally
 cloned into pORI/XhoI sites using the following 5'
 adapter: GGTACGAG(G). Size-selected 500bp for average
 insert size 1.8kb. Library constructed by Ling Hong in
 the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC library."

BASE COUNT 211 a 245 c 194 g 257 t
 ORIGIN
 Alignment Scores:
 Pred. No.: 4,760/144 Length: 897

Score: 1427.00 Matches: 245
 Percent Similarity: 95.90% Conservations: 12
 Best Local Similarity: 91.42% Mismatches: 4
 Query Match: 80.48% Indels: 0
 DB: 14 Gaps: 0
 GS-99-624-670-64 (1 299) x 10298263 (1 897)
 QY 1 MetGlyHisPheAsnLeuSerLeuSerThrTyrIlePheGlyAlaThrLeuValLeuMet 20
 DB 96 AAGAAATTTTGAAGATCATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 149
 QY 21 ThrArgValLysGlyIlePheLeuAspAsnTyrIleProSerPheValCysSerVal 40
 DB 150 ATATAGTATAGAGATGATTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 209
 QY 41 IleTyrLeuLeuValTyrPheGlyTyrMetLysAsnArgGluProPheSer 60
 DB 210 ATATATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 269
 QY 61 CysArgGlyIleLeuGlyLeuTyrAsnLeuSerLeuSerThrTyrMetPhe 80
 DB 276 TGGCGGGGGATTTTATGAGGTATAGCTTGGATTCATACAGAGTCTTGTATATGTTTC 429
 QY 81 TyrGluValThrGlyValTyrPheGlyTyrMetLysAsnArgGluProPheSer 100
 DB 340 TGTGAGTTAGTAAACAGAGTATGAGAGGAAATATAATTTCTTCTTCTTCTTCTTCTT 489
 QY 101 SerAlaGlyGluSerAspMetLysIleValValLeuTyrTrpTyrTyrPheSerLys 120
 DB 390 AATGCAAGCAAAATACAAATGAAATATGAGAGTCTTGTATGAGTCTTGTATGAGTCT 449
 QY 121 LeuIleGluPheMetAspThrPhePheIleLeuAlaGlyAsnAsnIleIleThr 140
 DB 450 CTATATAAATTTATGAGACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 509
 QY 141 ValLeuHisValTyrHisHisAlaThrMetLeuAsnIleTrpTrpPheValMetAsnTrp 160
 DB 510 GTCTGAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAGTAT 569
 QY 161 ValProCysGlyHisSerIlePheGlyAlaThrLeuAsnSerIleHisValLeuMet 180
 DB 570 GTCCCTCGGGGACTTATTTGGTGGCCACATTAATATAGTTCATGACAGGCTCATG 629
 QY 181 TyrSerTyrTyrGlyLeuSerSerIleProSerMetAlaProTyrLeuTyrTrpLysLys 200
 DB 650 TACTCTTACTATGGTTTGTGTACCTCCCTCCATGCTGCATACCTCTGGTGGCAAG 689
 QY 201 TyrIleThrGlyLeuValGlyPheValLeuThrIleIleGlyThrThrCysGly 220
 DB 690 TATATCATCATGAGGCAATCTTATTTATTTATTTATTTATTTATTTATTTATTTAT 749
 QY 221 ValPheThrProCysSerPheProValGlyPheThrIleGlyThrThrCysGly 240
 DB 750 GTCACTGCTGCTGCAATTCCTCTGTTGGTGTGA TTTCAGATTGATATCATGATT 809
 QY 241 SerLeuIleAlaLeuPheThrAsnPheTyrIleLeuThrTyrAsnLysLysGlyAl 269
 DB 816 TCCCTGATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 869
 QY 259 AsnArgLysAsp 264
 DB 870 TTCCGGGAGGAGAGAA 885
 RESULT 5
 A514872
 LOCUS
 DEFINITION A514872.1 111 NP1006 P12 Homo sapiens cDNA clone cl0080142P12 5
 patient mRNA sequence.
 ACCESSION A514872
 VERSION A514872.1 GI:12778465
 KEYWORDS EST.
 SOURCE human.

[illegible]


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BQ936171
LOCUS      BQ936171
DEFINITION AGNCOURT_B857100 NCI_CGAP_Mam2 Mus musculus cDNA clone
IMAGE:6441266 5' mRNA sequence.
ACCESSION BQ936171.1 GI:22461554
VERSION    BQ936171.1
KEYWORDS   EST.
SOURCE     house mouse.
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sclerogomathi; Muridae; Murinae; Mus.
REFERENCE  1 (bases 1 to 961)
            NIH-MC-171-251 NIH.
            TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
            JOURNAL     Unpublished (1999)
            COMMENT     Contact: Robert Strausberg, Ph.D.
                        Email: ecapbs@mail.nih.gov
                        Tissue Procurement: Gilbert Smith, Ph.D.
                        cDNA Library Preparation: Life Technologies, Inc.
                        cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                        DNA Sequencing by: AccuCourt Bioscience Corporation
                        Clone Distribution: MGC clone distribution information can be
                        found through the I.M.A.G.E. Consortium/LLNL at:
                        http://image.llnl.gov
                        Plate: LLNL1964 row: d column: 04
                        High quality sequence stop: 530.
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                        /clone="IMAGE:6441266"
                        /tissue="tumor, biopsy sample"
                        /dev_stage="5 months"
                        /lab_host="DH10B"
                        /note="Organ: mammary; Vector: pCMV-Sport6; Site:1; Salt:
                        Site_2: Not; Cloned unidirectionally. Primer: Oligo dT.
                        Library constructed by Life Technologies. Investigator
                        providing samples: Gilbert Smith, NIH"
BASE COUNT 212 a 279 c 242 g 238 t
ORIGIN
Aliquiment Scores:
Prod. No.: 4,286,125 Length: 961
Score: 1161.00 Matches: 232
Percent Similarity: 94.72% Conservativeness: 1
Best Local Similarity: 94.41% Mismatches: 6
Query Match: 70.50% Indels: 8
DB: 14 Gaps: 0
US-09-624-670-64 (1-299) X BQ936171 (1-961)
QY 60 SerCysAsqGlyTLeuGAGTLeuTyTAsnLeuGlyLeuThrlLeuLeuSerLeuTyTMet 79
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DB 1 TCTTCGAGGACATGCTGAGTTGAT-AACTTGAGTACACCTGCTGTCCTACATG 59
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QY 90 PheTyTGlutLeuValThrValThrValThrGlyLysTyTAsnLeuPheCysGlnGlyThr 99
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DB 60 TCTATGAGTGTGTCGACACGCTGTGTGGAGAGGAAATATAGAACTTTTCTGACGAGAA 119
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QY 100 ArgSerAlaGlyLysSerAspMetLeuGlyLeuValLeuThrPheTyTThrPheSer 119
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DB 120 CGCAGCGCGGAGAAACCGAATACAGACATGATCTGGCTCTCTGGGGGAGTACTTCCTCC 179
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QY 120 LysLeuThrLeuThrMetLeuThrPhePheThrLeuAlaAlaAsnAdhMissile 139
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DB 180 AAATCATCGAATTCATGAGAACCTTTTCTTCATCTCTGCAAAACAAACACCGAGATC 249
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QY 140 ThrValLeuHisValThrHisHisAlaThrMetLeuAsnLeuThrPheValMetAsn 159
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DB 240 ACCGTGTCATGTCATGACACACGACGATCATGTTAAATCTGCTGCTTTCTGATGAAC 299
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160 TrpValProCysGlyHisSerTyTPhaGlyValThrlLeuAsnSerPheThrHisValLeu 179
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DB 300 TGGTTCCTCCCGGCAATTCATATTTTGGTGGACATCAAAAGTTCATCACTCACTCCCTC 359
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DB 420 AAGTACATCACTCAAGCGGACGCTGGCTCCAGTTCTGTCTGACAAATATCTACAGACCTCC 479
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QY 220 GlyValPheThrPheGlySerPheThrLeuGlyLeuThrPhePhePheGlnThrGlyTyTMe 239
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DB 440 GGGCTCTTCCGCGCATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 539
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QY 234 ThrSerGln ThrAlaLeuPheThrAsnThrTyTThrGlnThrTyTAsnLys LysGly 258
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QY 259 AlaSerArg-ArgLysAspHisLeuLysGlyHisGlnAsnGlySerValAlaAlaValAs 278
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DB 600 GGCCTCTCGGAGGAGAAACACCTGGAGCGGCTACCAACAGGCTCTCTGCGGCGCTGCA 659
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QY 278 nGlyHisThrAsp-SerPheProSerLeuGlyAlaAsnGlyVal LysPheArgLysGlnArg 297
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DB 660 GGCACACACCAACAAGCTTCCTCTGCAAAACATGCTGCAAAATCTACGAAATCTACGAAACAC 719
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QY 297 gLys 298
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DB 720 GAAA 724
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B853179
LOCUS
DEFINITION 603375527E1 NCI_CGAP_Mam3 Mus musculus cDNA clone EST:1096712001
B853179
VERSION B853179.1 GI:15993926
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sclerogomathi; Muridae; Murinae; Mus.
            1 (bases 1 to 875)
            NIH-MC-171-251 NIH.
            TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
            JOURNAL     Unpublished (1999)
            COMMENT     Contact: Robert Strausberg, Ph.D.
                        Email: ecapbs@mail.nih.gov
                        Tissue Procurement: Lothar Hennighausen Ph.D., Ohio State Univ.
                        cDNA Library Preparation: Life Technologies, Inc.
                        cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                        DNA Sequencing by: Life Technologies, Inc.
                        Clone Distribution: MGC clone distribution information can be
                        found through the I.M.A.G.E. Consortium/LLNL at:
                        http://image.llnl.gov
                        Plate: LLNL1993 row: c column: 07
                        High quality sequence stop: 792
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                        /tissue="tumor, gross tissue"
                        /dev_stage="10 months"
                        /lab_host="DH10B"
                        /note="Organ: mammary; Vector: pCMV-Sport6; Site:1; Salt:
                        Site_2: Not; Cloned unidirectionally. Primer: Oligo dT.
                        Library constructed by Life Technologies. Investigators
                        providing samples: Lothar Hennighausen/Ohio State Univ, NIH

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Reference for transgenic model: Xu et al., Nature Genetics

22: 37-43 (1999).

BASE COUNT 188 a 256 c 191 q 240 t

ORIGIN

Alignment Scores:

Pred. No.: 1-90-124 Length: 875

Score: 1158.00 Matches: 244

Percent Similarity: 92.57% Conservativity: 5

Best Local Similarity: 90.71% Mismatches: 14

Query Match: 70.14% Indels: 12

DB: 13 Gaps: 0

US-09-624-670-64 (1-299) x H1853179 (1-875)

QY 1 MetGluHisPheAspAlaSerLeuSerThrTyrPheLys--AlaPheLeuLeuValProArgA 20
 DB 85 ATGGAACATTTTCATGCTCAGTCACTACCTATTTCGAATGGCCCTTCCTGGCCCGAG 144
 QY 20 sPThrArgValLysGlyTrpPheLeuLeuAspAsnTyrIleProThrPheValCys-Ser 39
 DB 145 ATACAGAGTCAGAGGATGGTCTCTCTGGACATTACATCCCTACGTTTCTGTCTCT 204
 QY 40 Val-IleTyrLeuLeu-IleValTrpLeuGlyProLysTyrMetLysAsnArgGlnProp 59
 DB 205 GTTAGTTTACTTACATACATTCATGCTGGGACCAATAATACATGAAGACCGGCGGT 264
 QY 59 heSerCysArgGlyIleLeuGlnLeuTyrAsnLeuGlyLeuThrLeuLeuSerLeuTyrM 79
 DB 265 TCTCTTGGGAGGCAATCTGAGTTGTATACCTTGGACATCAACCTGCTGCTCTCTCT 324
 QY 79 ethcTyrGluLeuValThrGlyValTrpGlyValTrpGlyLysTyrAsnPhePheCysGlnClyt 99
 DB 325 TCTTATGAGTGGTGGTAACTGTCTGTGAAAGGAAAFATATTTCTGGTGGAGGAA 384
 QY 99 hrArgSerAlaGlyGluSerAspMetLysIleIleArgValLeuTrpTrpTyrTyrPheS 119
 DB 385 CACGCGAGCGGAGCAATCCGATAGAAGATCATCCCGCTCTCTGGCTGCTACTCTCT 444
 QY 119 erLysLeuIleGluPheMetAspThrPhePhePheIleLeuArgLysAsnHisGlnI 139
 DB 445 CCAAACTATCAAAATCAATGACATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 504
 QY 139 leThrValLeuHisValTyrHisHisAlaThrMetLeuAsnIleTrpTrpPheValMetA 159
 DB 505 TCAAGCTATCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 564
 QY 159 snTrpValProCysGlyHisSerTyrPheGlyAlaThrLeuAsnSerPheIleHisValI 179
 DB 565 ACTGCTTCT 624
 QY 179 euMetTyrSerTyrTyrGlyLeuSerSerIleProSerMetArgProTyrLeuTrpTrpL 199
 DB 625 TTAGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 684
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 QY 219 CysGlyValPheTrpProCysSerPheProLeuGlyTrpLeuPhePheGlnIleClyTyr 238
 DB 744 TGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 798
 QY 239 MetIleSerLeuAlaLeuPheThrAsnPheTrpIleGlnThrTyrAsnLysLysGly 258
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 DB 859 CT-TCTCGAGAAAAA 872

RESULT 14
 HQ213770

LOCUS

DEFINITION

5', mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BQ213770

AGENCIPT_708012 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6064578

BQ213770

BQ213770.1 GI:20395170

EST.

human.

Homo sapiens

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,

Mammalia: Eutheria: Primates: Catarrhini: Hominoidea: Homo.

1 (bases 1 to 897)

NIH-MGC <http://mgc.nci.nih.gov/>

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgabbs-remail.nih.gov

Tissue Procurement: ATCC/DC/DT/

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at:

<http://image.lln.gov>

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High quality sequence stop: 625.

Location/Qualifiers

1..897

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/lab_host="DH10B (phage-resistant)"

/note="Organ skin, Vector pCMV Sport6, Site 1: Nott,

Site 2: Sall, Cloned unidirectionally. Primer, Oligo dt.

Average insert size 2 kb. Library constructed by Life

Technologies."

BASE COUNT 212 a 233 c 198 g 253 t 1 others

ORIGIN

Alignment Scores:

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Score: 1152.00 Matches: 213

Percent Similarity: 94.12% Conservativity: 11

Best Local Similarity: 89.50% Mismatches: 9

Query Match: 69.78% Indels: 5

DB: 14 Gaps: 1

US-09-624-670-64 (1-299) x BQ213770 (1-897)

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DB 84 ATGGAACATTTTCATGCTCAGTCACTACCTATTTCGAATGGCCCTTCCTGGCCCGAG 143

QY 21 ThrArgValLysGlyTrpPheLeuLeuAspAsnTyrIleProThrPheValCysSerVal 40

DB 144 ACTAGAGTAAAGAAAGAGGATGGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 203

QY 41 IleTyrLeuLeuIleValTrpLeuGlyProLysTyrMetLysAsnArgGlnProPheSer 60

DB 204 ATATATTTTACTAATTTGTATGCTGGACCAAAATACATGAGGAATAAACAGCCATTCTCT 263

QY 61 CysArgGlyIleLeuGlnLeuTyrAsnLeuGlyLeuThrLeuLeuSerLeuTyrMetLys 80

DB 264 TGGCGGAGGAGATTTTATGCTGATATAAATTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 323

QY 81 Ty-GluLeuValThrGlyValTrpGluGlyLysTyrAsnPhePheCysGlnGlyThrArg 100

DB 324 TGTGAGTTAGTAAACAGGAGATGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 383

QY 101 SerAlaGlyGluSerAspMetLysIleIleArgValLeuTrpTrpTyrTyrPheSerLys 120

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QY 141 ValLeuHisValIleHisHisAlaThrMetLeuAsnIleThrPheValMetAsnTrp 160
DB 504 GTCCTGCACGCTAACCAACATGCTCAACATGCTGCTGCTGCTGCTGCTGCTGCT 563

QY 161 Val-ProCysGlyHisSerTyrPheGlyAlaThrLeuAsnSerPheIleHisValLeuMe 180
DB 564 GTCCTGCACGCTAACCAACATGCTCAACATGCTGCTGCTGCTGCTGCTGCTGCT 623

QY 180 TTTTSCrTyrTyrTyrGlyLeuSerIleProSerMetArgProGlyLeuTrpIlePhe 200
DB 624 GTACTCTTATGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 683

QY 200 STTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 220
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ACCESSION BED0106
VERSION BED0106.1 GI:8470494
KEYWORDS EST.
SOURCE human.
ORGANISM Homo Sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 661)
Dias Neto, E., Garcia Correa, K., Verjovsky-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zado, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brunstein, A., de Oliveira, F.S., Bucher, F., Junqueira, C.V., O'Hare,
M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7): 3491-3496 (2000)
29282663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11 2704922
Fax: +55-11 2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAHPSP/LICR Human Cancer Genome
project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?J=612 RC4-BT0629 120
290-911-302K13 2000 02 15K14-1)
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/dev_stage "Adult"
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Small; A mini library was made by cloning products derived
from cRESTES PCR (U.S. Letters Patent application No. 196
7716 Ludwig Institute for Cancer Research) profiles
into the puc 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low

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BASE COUNT 159 a 165 c 143 g 194 t
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Best Local Similarity: 99.47% Mismatches: 4
Query Match: 69.05% Indels: 0
Gaps: 0
DB: 10

US 09-624-670-64 (1 299) x BE080106 (1 661)

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QY 38 CysSerValIleGlyLeuLeuIleValIleValIleValIleValIleValIleVal 57
DB 73 TGGCTCTGATATATTAATAATGATGATGATGATGATGATGATGATGATGATGAT 132

QY 58 ProPheSerCysArgGlyIleLeuGlnLeuLeuTyrAsnLeuGlyLeuThrLeuLeuSerLeu 77
DB 143 CCATCTCTTCCGCGCGGATTTAGTGGTGATAAAGCTACATCAATCAATCAATCAAT 192

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DB 153 TATATGTTCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 252

QY 98 GlyThrArgSerAlaGlyGlySerAspMetLysIleLeuValIleLeuIleThrTyrTyr 117
DB 253 GGTACACAGCAATGCAAGAAATCAGATATGATGATGATGATGATGATGATGATGAT 412

QY 118 PheSerLysLeuIleGluPheMetAspThrPhePhePheIleLeuArgLysAsnHis 137
DB 313 TTCCTCAACATCATAGAAATTTATGCGACATTTCTCTCTCTCTCTCTCTCTCTCTCT 472

QY 138 GlnIleThrValLeuHisValTyrHisHisAlaThrMetLeuAsnIleTyrTrpPheVal 157
DB 373 CAGATACAGGCTCTGACATGATGATGATGATGATGATGATGATGATGATGATGAT 432

QY 158 MetAsnTrpValProCysGlyHisSerTyrPheGlyAlaThrLeuAsnSerPheIleHis 177
DB 433 ATGAATCTGGCTGCGCTGCGGCACTTATTTGGTGCAATATATATATATATATATAT 492

QY 178 ValLeuMetTyrSerTyrTyrIleLeuSerSerIleProSerMetArgProTyrLeuTrp 197
DB 493 GTCCTCACTGATCTTACTAAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 552

QY 198 TrpLysLysTyrIleThrGlnGlyGlnLeuValGlnPheValLeuThrIleIleGlnThr 217
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